Phylogenetics and systematics of North-African Geckos *Tarentola*

Von der Fakultät für Lebenswissenschaften

der Technischen Universität Carolo-Wilhelmina

zu Braunschweig

zur Erlangung des Grades eines

Doktors der Naturwissenschaften

(Dr. rer. Nat.)

genehmigte

Dissertation

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aus Tajura / Libyen

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Eingereicht am: 21.03.2011

Mündliche Prüfung (Disputation) am: 14.06.2011

Druckjahr 2011

Vorveröffentlichungen der Dissertation

Teilergebnisse aus dieser Arbeit wurden mit Genehmigung der Fakultät für Lebenswissenschaften, vertreten durch den Mentor der Arbeit, in folgenden Beiträgen vorab veröffentlicht:

Publikationen

Joger, U., Bshaena, I. : A new *Tarentola* subspecies (Reptilia: Gekkonidae) endemic to Tunisia. Bonn Zoological Bulletin 57 (2): 267-247 (2010).

Tagungsbeiträge

Bshaena, I & Joger, U. : Phylogeny and systematics of North African *Tarentola*. (Vortrag). Deutsche Gesellschaft für Herpetologie und Terrarienkunde (DGHT) Nachzuchttagung Deutscher Herpetologentag, September (2009).

ACKNOWLEDGEMENTS

First of all I wish to express my sincere gratefulness to Allah, without his help this work would not been done.

I would like to express my gratitude to many individuals who assisted me throughout the course of my doctoral research. First, I would like to express my appreciation to my supervisor, Prof. Dr. Ulrich Joger for his kind supervision, sincere help, fruitful discussion, an open ear and for the extraordinary advice, caring, encouragement, and affection he bestowed on me.

My sincere thanks go to Prof. Dr. Miguel Vences for the opportunity of participating in this project, to work in his laboratory, and offered numerous critical comments which contributed to improve the study.

I am also very grateful to Prof. Dr. Dirk Selmar, who kindly agreed to become a member of the dissertation committee.

I am much obliged to several people who contributed in sample material or helped to make sample material available for me. I am grateful to all people in Libya who help me in field work for catching Lizards.

Many thanks go to all our laboratory technicians group who help me in the first period in the laboratory work.

In addition, I would like to thank all my colleagues for his kindly suggestions and discussions.
My special thanks go to my wife Asya Swiddan for her patient love and my pretty kids Mustafa, Nada and Shahin for their lovely smiles that can relieve any kind of tiredness.

I am greatly thankful to my mother for her heartily feelings, unconditional support and constant prayers.

My huge thanks go to my brothers, especially Usama for his support and managing our business in Libya during my PhD study

Braunschweig, 16.03.2011

Ismail Mustafa Bshaena

Contents

List of Figures

List of Tables

I dedicate this work to the soul of my father who passed away years ago, and I hope my God bless him.

01 GENERAL INTRODUCTION

1.1. Introduction

The diversity of life is amazing. More than two million existing species of plants and animals have been named and described; many new species remain to be discovered, as a minimum ten million according to most estimates (Wuketits & Ayala, 2005). What is impressive is not just the number but also the incredible heterogeneity in size, shape, and ways of life. These variations on life are the outcome of the evolutionary process. All organisms are related by descent from common ancestors: for example, mammals, birds, reptiles, amphibians, and fishes share as ancestors small worm-like creatures that lived in the world´s oceans 600 million years ago (Mya). Because of biological evolution, lineages of organisms change over time; diversity arises because lineages that descend from common ancestors diverge over the generations as a result of adaptation to different styles of life, the variation in phenotype is a result of interaction of genotype and the environment.

An important innovation in biological sciences in the 20th century was the introduction of phylogenetic systematics (or cladistics) by Willi Hennig (1950). The main principle of cladistics is that all observed morphological or other biological features of organisms have to be translated into discrete characters, that a have alternative expressions.

The observation, description, and understanding of morphological characters, with the data provided by the fossil record were until recently the only data set available to infer evolutionary history of organisms. The scarcity of direct information about the history of life has long frustrated evolutionary biologists. To understand how evolution occurs, it is necessary to know not only the character states of living organisms, but also of their ancestors. Although the fossil record is rich with examples of evolutionary transformations, but enough fossils are not available from many taxa and character states. In the second half of the last century, the biochemical characterization of proteins contributed new data sets

for biologist; today the combination of morphological methods with molecular methods provides powerful approach to understanding the evolution and geographical distribution of organisms. With the discovery of polymerase chain reaction (PCR) technology by Mullis in the late 70´s of the last century, introduced to scientific community by Mullis & Falonna (1987), and the introduction of mitochondrial DNA (mtDNA) markers, all these helped to obtain a fuller picture of the evolutionary history of organisms (Zhang & Hewitt, 2003). Enormous amounts of data become reachable; modern automated sequencers allow reading more and more base pairs, consequently, the number of known nucleotide sequences increases exponentially, in addition to the number of research papers which infer phylogenetic relationships on the basis of sequence data, too. While the impact of morphology, biochemistry, and specially the fossil record data for phylogenetical and systematical purposes diminishes; the molecular data become accessible. By the huge number of sequence data on the one hand, and the fast computerized analytic methods on the other hand, molecular phylogenetic studies grow to be more precisely, it is almost completely unbiased. Recent years have seen an enormous growth in phylogenetic studies based on molecular data, many of which are concerned with closely related species or variation within species. In particular, the use of mitochondrial DNA as a molecular marker has considerably improved our knowledge about past events shaping the genetic diversity within species.

Mitochondrial DNA: as it is known, the mitochondrion is a membrane-bound cytoplasmic organelle present in all eukaryotic organisms that is responsible for respiration and the production of energy. Contained inside the mitochondria is a loop of DNA that is copied and transferred from generation to generation independently of the nuclear genomes (Appleton, 2003). And it is inherited maternally as it is transmitted across generations as a maternal lineage (there are very rare exceptions). Vertebrate mtDNA is thought to evolve about 1-2%/10^6 years although the rate may vary among taxa (Brown, 1985; Brown et al., 1979). mtDNA is histone-free, has limited repair ability and a relatively high mutation-

fixation rate and thus, evolves 5-10 times faster than the nuclear genome. The mtDNA genome of most vertebrates consists of a closed circular DNA molecule of 16,000-18,000 base pairs (Cantatore and Saccone 1987). There are several reasons why molecular data, particularly DNA and amino acids sequence data, are much more suitable for evolutionary studies than morphological and physiological data. These are summarized in Nei and Kumar (2000) as follows: First, DNA and protein sequences are strictly heritable units; this may not be true for many morphological characters that can be influenced to varying extents by environmental factors. Second, the description of molecular characters and character states is unmistakable; for instance, the third amino acid in the preproinsulin of the rabbit (*Oryctolagus cuniculus*) can be unmistakably identified as serine, and the homologous position in the preproinsulin of the golden hamster (*Mesocricetus auratus*) as leucine; in contrast, morphological descriptions normally contain such unclear modifiers as ‘‘thin, reduced, slightly elongated, partially enclosed, and somewhat flattened’’. Third, molecular characters commonly evolve in a much more regular manner than do morphological and physiological characters, and as a result can provide a clearer picture of the relationships among organisms. Fourth, molecular data are often much more agreeable to quantitative analysis than are morphological data. In fact, complicated mathematical and statistical theories have been developed for the quantitative analysis of DNA sequence data, whereas morphological studies retain a great deal of qualitative argumentation. Fifth, homology assessment is easier with molecular data than with morphological traits. Sixth, their marvelous scope of variation ranging from very variable to very conservative such that some molecular data can be used to assess evolutionary relationships among very distantly related organisms. For example, numerous protein and ribosomal RNA sequences can be used to reconstruct evolutionary relationships among such distantly related organisms as ‘‘fungi, plants, and animals’’. On the contrary, there are few morphological characters that can be used for such a purpose. Finally, molecular data are much more abundant than morphological data; this abundance is especially useful when working with organisms such as bacteria,

algae, and protozoa, which have only a limited number of morphological or physiological characters that can be used for phylogenetic studies. The high frequency of mtDNA alleles within species is thought to be result from four primary characteristics of the mitochondrial genomes: 1) high mutation rate; 2) absence of recombination; 3) reduced effective of population size (because of its being haploid and maternally inherited); 4) in addition to maternal transmission (Gemmell et al., 2004).The mtDNA gene pools of animals and plants are often subdivided into clines of phylogenetically related haplotypes that show no or little overlap in their geographical occurrence (Avise et al., 1979; Avise 2000), a phenomenon that gave rise to the discipline of Phylogeography. In particular, mtDNA analysis has become established as a powerful tool for evolutionary studies of animals, mtDNA sequence data have used to provide insights into population structure and gene flow, hybridization, phylogenetic relations, biogeography and also for identification of subspecies and species; the use of mitochondrial DNA as a molecular marker has considerably improved our knowledge about past events shaping the genetic diversity within species (Brown et al, 1982; Moritz et al, 1987; Wan et al, 2004).

As explained above, variation in mtDNA has been used extensively to map genetic variation of natural populations (Avise, 2000). Phylogeography which combines phylogenetics and biogeography is the examination of geographic distributions of evolutionary lineages to understand the evolutionary history of a taxon (Manel et al, 2003). It is also, a comparison of the genealogy of lineages with the geographic distribution patterns of the population; Phylogeographic analysis provides conclusions into the effects of geographic structures on genetic fragmentation of populations (Avise et al, 1987). These barriers for example: rivers, plains, mountains, volcanism and/or glacial activity may have a deep effect on the distribution of genetic variation across large geographic scales (Hewitt, 1996). Phylogeographic investigations are restricted mainly to species or species complexes, and the time scale is usually limited to approximately the last 2-3 Mya, the Quaternary (or the Pleistocene), and therefore small compared with studies on generic or higher taxonomic level (Huang et al, 2004).

During Pleistocene the earth experienced several glacial cycles (ice ages), these cycles are characterized by dramatic climatic fluctuations, the last 700 thousand years (Kyrs) thereof seeing extreme climate oscillations where shorter warm periods (interglacial's) have been succeeded by longer periods of colder climates (glacials), each lasting around 100 kyrs, interrupted with interglacial periods, every lasting around 10-20 kyrs; the latest glacial ended about 12 kyrs ago and was followed by warmer interglacial of today, the Holocene. Throughout Pleistocene, this period of the earth history was distinguished by massive accumulation of ice-sheets (glaciers) during the cold cycles in the northern hemisphere where almost big area of the earth´s total land surface was covered by permanent glaciers. The ice-sheets covered particular northern Europe, northern portion of North-America, Siberia, and several mountainous regions (Nilsson, 1983; Brown & Lomolino, 1998; Webb & Bartlein, 1992). The consequences of the Quaternary climate have obviously been dramatic effects for most organisms, causing a variety of expansions (or contractions) and distribution shifts, where temperate species retreated southwards to refugial areas during glacials and claimed the habitats we find them in today only after the cold period ended; for that reason, the effects on genetic variation must have been deep (Brown & Lomolino, 1998). The attention to phylogeographic research has been considerable over the last decades, with the advent of easily applied molecular tools; researchers have been given the opportunity to describe the genetic variation of species (Avise, 1998).

1.2. Family: Gekkonidae Gray, 1825

The fossil records show significantly that Reptiles were in the past more numerous and diverse than they are today (Cogger & Zweifel, 1998), there is in general more than 8000 species of Reptiles (class: Reptilia) which consist of four orders, 64 families, and about 900 genera. Gekkonidae is one of largest vertebrates group, a relatively basal lineage among squamates (Vidal & Hedges, 2005), and the only major lineage of primarily nocturnal lizards (Pianka & Vitt, 2003), it is also one of the well known families of Reptiles. Geckos and Pygopods comprise the Gekkota, one of three major lineages of living lizards, more than 25% of all living genera and species of lizards are placed in this family (Kluge, 1987). There are four subfamilies of the Gekkonidae (Diplodactylinae, Gekkoninae, Eublepharinae, and Sphaerodactylinae). There is diversity recognized, anyway we can discriminate about 1130 species in 108 genera (Kluge, 2001; Bauer, 2002; Han, Demin et at, 2004) and many new taxa are described every year. The family is distributed throughout the world on all major land masses and almost all oceanic islands, it is the most adaptable and geographically widespread family, geckos are found in tropics, subtropics and some warm temperate areas, some species range as far north as the southern United States of America, southern Europe, and southern Siberia. To the south, geckos extend to reach New Zealand and southern tip of South America (Feng et al, 2007).

The distribution of gecko lizards on continents in the southern Hemisphere is presumed to have been heavily influenced by Gondwanan vicariance (Cracraft, 1974; Bauer, 1990, 1993) and the ancient origin of geckos 165–180 Myra (Kluge, 1987) makes this a believable scenario.

The geckos are masters in the art of adaptation, they mostly live in trees, but they can occupy an extensive array of habitat types; the variety of form and degree of specialization of its members reflect a diversity of niches. Geckos have high diversity in arid and semiarid habitats in Africa, Australia; they are well

distributed and/or diversified in arid regions because of their special capacity for adaption with harsh desert condition (Baha El Din, 2006; Starosta et al, 2004). Although geckos are mostly common at lower elevations, they are also found in high elevations. Most geckos are nocturnal. They stay during the day under trees or in tree hollows, under rocks. In the early evening they come out to look for prey. Diurnal species are mostly active in the late morning and middle of the afternoon. In tropical regions which are warm throughout the year, geckos stay active all the time. In other regions, geckos enter burrows or rock cracks and remain there most the time during the cool season. Geckos normally live by themselves, only a few species live in groups. They all are insect eaters, some diurnal species show a marked preference for flower nectar; there are some exceptions (see figure 1), more recently, the predation of gecko *Tarentola annularis annularis* on small mammals was recorded (Crochet & Renoult, 2008). Gecko males defend their feeding and resting places by using warning sounds, often many clicks and chirps (which is extremely rare for a reptile), in Asia, the clicks of Tokee can be heard over a distance of about a hundred meters (Starosta et al, 2004) . Defense strategies include running away; squirting a sticky fluid at predators, or animals that hunt them to eat them; biting; and dropping their tails. A gecko's tail will continue to wriggle after it is shed, fooling the predator and allowing the gecko to escape. Some gecko species are also able to shed body skin if they are grabbed by other animals, this skin regrows, as does the tail. Most geckos' lay two eggs in each reproductive cycle, few species are viviparous.

Figure 1. An adult *Tarentola annularis annularis* in *Acacia* tree holding its prey, small mammal [gerbil]. Source: Crochet & Renonlt, 2008.

Gekkonidae lizards have several unique features (apomorphic characteristics). They are small to medium size lizards. While most geckos are brown, gray, or black (drab in color, in accordance with nocturnal habits), a few are yellow, orange, red, blue, or green (diurnal geckos, tend to have brighter colors). They may have stripes or spots, colors on the head and neck may be different from the colors on the back. Geckos have stocky, flattened bodies, short necks and wide flat heads; the body is covered by soft skin with sparse horny tubercles, their skin structure provides them protection against heat, dryness and sunlight. They have four well-developed short limbs (legs); each limb has five toes (digits). The toes usually have transverse rows of hooked lamellae for adhesion, and some species have claws on each foot. The feet are one of the most striking and varying aspects of the morphological characteristics of the gecko. While Diplodactylines, Eublepharines and some Gekkonines have slender digits with well-developed claws, many species have expanded pads on the base and/or tips of the toes that permit adhesion to smooth surfaces. The presence of this highly complex adhesive digital system enables geckos to climb on any surface (they can run easily on a glass plate or vertical clammy surface); they are often described as good climbers. But some geckos are ground-dwelling (Glaw et al, 2007). Most members of this family are distinguished from other lizards by presence of large eyes that are open all the time. Except for a few species, the eyes don't have mobile eyelids; instead the eyes are protected by a fixed transparent spectacle (clear see-through scales). Geckos clean these scales regularly with their long tongues. Most geckos are nocturnal so their pupils are narrow with vertical slit to block out light, the rest have round pupils in the center of their eyes (diurnal geckos). Gekkonidae teeth are small in size, conical, pleurodont and they are from the similar type throughout the mouth (homodont), the anterior teeth are generally larger than the posterior teeth (Bauer, 1990).

1.3. Genus: *Tarentola*

The genus *Tarentola* (Reptilia, Gekkonidae), derived their name from the south Italian harbour Taranto or Tarentum (Schleich et al, 1996), according to the work of Joger (1984b), the first radiation of this genus started in Eocene times some 65 Mya, when Africa north of the rain forest belt had for the first time climatic condition suitable for this genus. In the Oligocene 33.7- 23.8 Mya the five subgenera had separated from each other, *Tarentola*, *Makariogecko*, *Sahelogecko*, *Saharogecko* and *Neotarentola* all having a common ancestor. This division into five subgenera was recognized according to different criteria, which were incorporated with the geographical distribution as well as environmental factors.

The genus *Tarentola* comprises of around 20 morphologically very similar species (Joger, 1984a-b-c; Schleich, 1984; Baha El Din, 1997; Sprackland & Swinney, 1998; Carranza et al, 2000; Harris et al, 2004), which live mainly in semi-arid to arid habitats. Its main distribution area lies in North Africa (north Africa is the center of diversity), coastal regions of Mediterranean sea (southwest Europe), Macaronesian islands (Selvages, Canaries, and the Cape Verde), and also Cuba and the Bahamas (see figure 2). The ancestors of the species found today on these widely dispersed oceanic islands probably reached there by passive rafting (Joger, 1984b; Carranza et al, 2000; Perea, Harris, 2008).

Geckos in genus *Tarentola* typically are nocturnal and inhabit dry, rocky areas (Andrew et al, 2006), *Tarentola* is an adaptable lizard that is found in rocky areas, deserts with firm ground, it can be found in drains under roads, ruins, old buildings in crevices and fissures, the nooks and crannies of the wall provide an ideal home for the lizards. It is also found close to sandy deserts with trees and in palm oasis. The female lies between four and six clutches of two eggs per year.

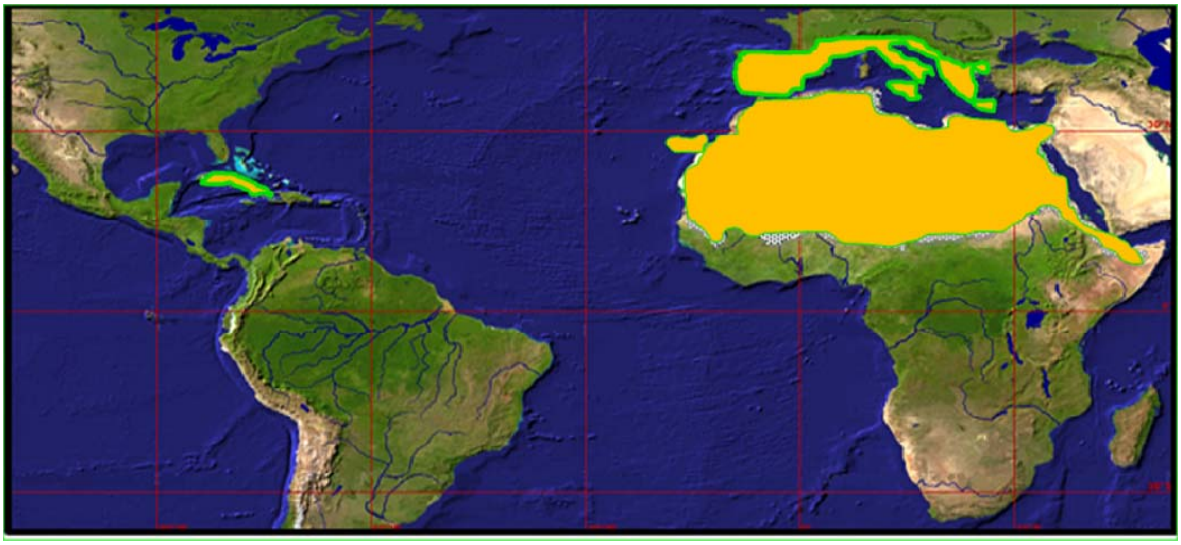

Figure 2. General distribution range of the genus *Tarentola.* Source modified after: Joger, 1984 a, b; Willand, 1997; Baha El Din, 2006.

The genus *Tarentola* has been intensively studied phylogenetically, as well as phylogeographically for some species. Previous studies, based on both morphological and molecular data have investigated the phylogenetic relationships of *Tarentola*. With using the classical morphological methods, scanning electromicroscopy of scales surfaces, and molecular analysis based on serum protein electrophoresis and quantitative precipitin tests of serum albumin (Joger, 1984c, 1985), and DNA sequences from mitochondrial and nuclear genes (e.g. Nogales et al, 1998; Gübitz et al, 2000; Carranza et al, 2000, 2002; Jesus et al, 2002, Harris et al, 2004a,b; Perea & Harris, 2008; James et al, 2009). Morphologically similar or conservative species have been shown to contain genetically distinct lineages (Carranza et al, 2000; Jesus et al, 2002). The sequence analyses combined the Old World species in a single group, leaving the New World species *T. americana* as the most divergent lineage in the genus. This also agrees with its placement as the sole representative of the subgenus *Neotarentola* (Joger, 1984). Systematically gecko *Tarentola* is a North African Clade, *Tarentola mauritanica* (Moorish gecko) in North Africa appears to be highly divergent, and represents a species complex with at least eight different

mtDNA lineages (Harris et al, 2004a,b). Therefore *Tarentola* has invaded many of the warmer Islands in the North Atlantic Ocean.

There were four main invasions of archipelagos presumably by rafting (Carranza et al, 2000):

1) The subgenus *Neotarentola* reached Cuba up to 23 Mya; it seems that via North Equatorial current, trip of no less than 6000 km.

2) The subgenus *Tarentola* invaded the eastern Canary Islands relatively recently covering a minimum of 120 km.

3) The subgenus *Makariogecko* got to Gran Canaria and western Canary Islands 7 – 17.7 Mya, either directly from the mainland or via the Selvages or the archipelago of Madeira, an excursion of 200 – 1200 km.

4) A single species of *Makariogecko* from Gomera or Tenerife in western Canaries made the 1400 km journey to Cape Verde Islands up to 7 Mya by way of the south-running Canary current.

The key description of the genus *Tarentola* of North Africa (Table 1) represents the current state of knowledge before the present study is as follows:

Table1. Morphological key to different *Tarentola* species and subspecies in North Africa before our study. Source: modified after Schleich et al, 1996., Geniez et al, 1999., Joger, 1984a,b., Baha El Din, 2006.

1- Dorsal tubercles (at least the dorsolateral ones) frontally and laterally surrounded by a horseshoe shaped rosette of 5-8 symmetrically arranged secondary tubercles of different size. Interspersed diminished tubercles on the vertebral line, single or in 1-2 rows. 3
1[1]- Dorsal tubercles without rosettes; no small tubercles in the vertebral region: 2
2- Rostral reaching at least one nostril, or nostril surrounded by four scales and the first supralabial; 13-25 enlargened scales and lamellae in total under the first toe: 6
2[1]- Rostral reaching no nostril. Nostril surrounded by three nasel scales and the first supralabial; 11-13 enlarged scales and lamellae in toal under the first toe: *Tarentola neglecta* 8

3- Rostral reaching nostrils and/or tubercles with several keels **4**

3[1]- Rostral separated from nostrils and/or tubercles with simple keels **7**

4- Only lateral tubercles surrounded by rosettes; middorsal tubercles flat. 21-23 scales and lamellae in total under the 5th toe (to toe base): ***Tarentola boehmei***

4[1]- Lateral and dorsal tubercles surrounded by rosettes; middorsal tubercles high. 16-20 (rarely 21) scales and lamellae under the fifth toe: **5**

5- Basic colour whitish. Lateral tubercles spiny and directed caudally. Enlarged scales between dorsal and ventral scales: ***Tarentola mauritanica fascicularis***

5[1]- Basic colour grayish. Lateral tubercles pyramid-shaped. No enlargened scales between dorsal and ventral scales: ***Tarentola mauritanica juliae***

6- 1-3 enlargened scales rows between mental shield and gular scales. Normally 16 longitudinal rows of dorsal tubercles: ***Tarentola ephippiata hoggarensis***

6[1]- No enlarged intercaler scales between mantel shield and gular scales. Normally more than 14 longitudinal rows of dorsal tubercles: ***Tarentola annularis annularis***

7- 28-46 gular scales. 16-21 scales and lamellae under the 5th toe. Tubercles not radially striated. Basic colour gray. Iris grey in life: ***Tarentola mauritanica mauritanica***

7[1]- 46-59 gular scales. 21-25 scales and lamellae under the 5th toe. Tubercles radially striated. Basic colour whitish pink or light brown. Iris ochre in life: ***Tarentola deserti***

7[2]- 32-45 gular scales, 17-19 scales and lamellae under the 5th toe. Basic colour opaque dark grey. Iris pinkish-grey on life: ***Tarentola. m. pallida***

8- Less than 30 dorsal tubercles in one row from occiput to posterior angle of hind leg insertion. Ventral scales distinctly larger than dorsal ones: ***Tarentola neglecta neglecta***

8[1]- At least 30 dorsal tubercles in one longitudinal row. Ventral and dorsal scales about the same size: ***Tarentola neglecta geyri.***

9- On average 16 lamellae under the 5th, tubercles in temporal region indistinct, separated by subequal scales. Postmental much larger than gular; rostral excluded from nostril. General colour dark, iris ochre on life.

T.mindiae

1.3.1. Genus *Tarentola* in Africa and Maghreb countries

In the next pages a brief overview about the known species and subspecies of gecko *Tarentola* in Africa and Maghreb countries are given, which represent the current knowledge as understood before our study; it is based on most recent taxonomic literatures (secondary literatures not used), which is suited in the species account.

1.3.1.1. *Tarentola mauritanica* Linnaeus, 1758

Synonymies: *Gecko muricatus* Laurenti, 1768

Gecko stellio Merrem, 1820

Platydactylus muralis Dumeril & Bibron, 1836

Common name: Moorish Gecko, Crocodile Gecko

Four subspecies have been described:

1.3.1.1.1. *Tarentola mauritanica mauritanica* Linnaeus, 1758

Synonymies: *Platydactylus facetanus* Strauch, 1862

T. mauritanica var. mauritanica subvar. gracilis Doumergue, 1899

T. mauritanica var. mauritanica subvar. atlantica Doumergue, 1899

T.mauritanica var. saharae Doumergue, 1899

T.mauritanica var. lissoide Doumergue, 1899

Tarentola tuberculata Rosen, 1905

Distribution: The Moorish Gecko is distributed in Mediterranean regions, with a European range from Iberian Peninsula to Italy via south France and a few isolated populations extending further east in Yugoslavia, Greece and Crete and many Mediterranean Islands. In Africa, it is found in northern portion of the continent (see figure 3), from the north of the high Atlas mountains via northern Algeria (north of Sahara-Atlas), to north Tunisia (Joger, 1984a).

Diagnosis: A well-built gecko, total length up to 160 mm, SVL male 84 mm, female 75 mm; foreleg male 26.1 mm female 23.9 mm; hindleg male 29.9 mm, female 28.7 mm. With large expanded head, usually obtusely keeled scales, 13-16 interorbital scales. Nostril not in contact with rostral; anterior border of the ear-opening not denticulated. 34-45 gulars. Neck sides with rosettes of large conical tubercles surrounded by smaller ones; 10-16 dorsal rows of tubercles with rosettes, except 1-2 median ones. No enlarged tubercles at the border between

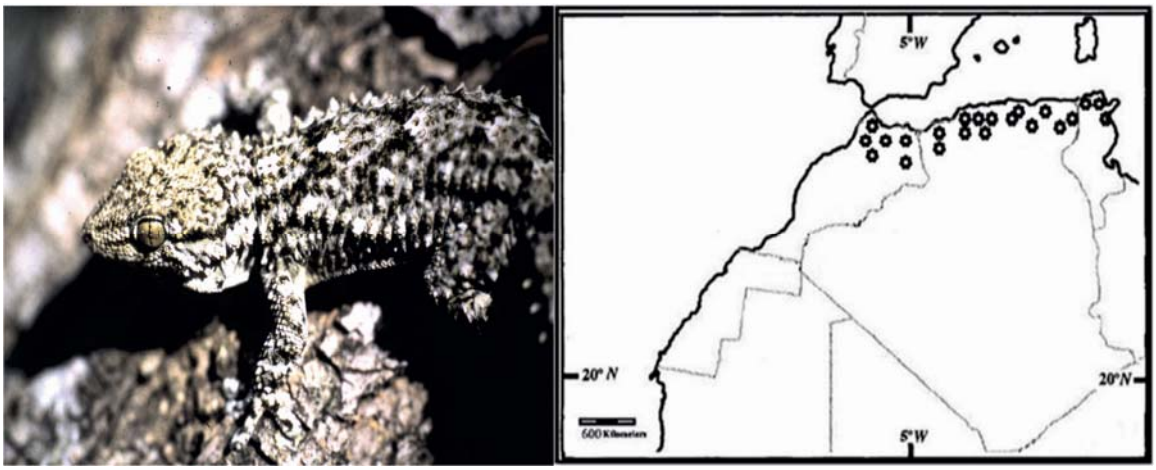

Figure 3. In the left photograph of an adult *Tarentola mauritanica mauritanica*, from Ifrane, Morocco. Source: photograph by U. Joger; and in the right side map shows the distribution range of this subspecies in Africa.

ventral and dorsal scales 4th to 6th row pointed; dorsal substantially smaller than ventral, sharply delimited. 3rd and 4th digits with visible claws, on other digits minute retractile claws in females, none in males. 18-21 scales and lamellae underneath the fifth toe.

Color pattern: Medium to dark gray or gray-brown (Colour change physiological: becomes lighter in darkness and dark while basking), with 4-5 dark transversal bands (counting from the neck until the sacral region) on both sides which disappear with age, and behind each connecting a bright spot. Iris is gray in live animals (Joger, 1984a; Scleich et al, 1996).

1.3.1.1.2. *Tarentola mauritanica fascicularis* Daudin, 1802

Synonymies: *T. m. mauritanica* Loveridge, 1947 (partim, non Linnaeus, 1768)

Distribution: Type locality: Tripoli: Neotype: from Ain Zeyanah, 20 km south of Banghazi, Libya, designated by Joger (1984a), is found in north Egypt and extends westward in a rather narrow band along the Mediterranean coast (see figure 4) across northern Libya and into southern Tunisia (Baha El Din, 2006; Joger, 1984a).

Diagnosis: Medium sized and robustly built lizard, total length reaches 160 mm; SVL reaching up to 84 mm by male, 75mm by female. Back and dorsal surface of

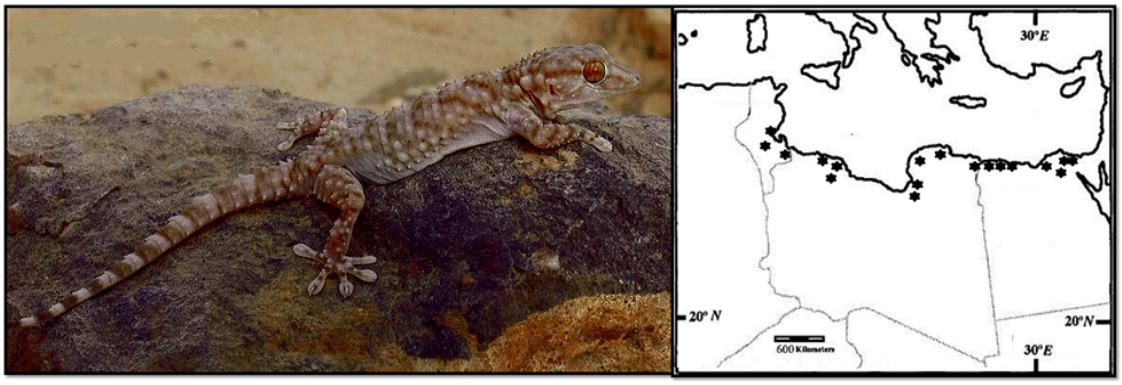

Figure 4. In the left photograph of an adult *Tarentola mauritanica fascicularis*, for Um Al-Araneb, Libya. Source: photograph by Adel Ibrahim; and in the right side map shows the distribution range of this subspecies.

tail covered with regular bands of sharply protruding tubercles. Tubercles have multiple keels and are surrounded by rosettes of 5-8 medium sized scales in [a horseshoe] like formation. Tubercles are separated laterally from each other by 4-5 small scales. They possess an average 17 lamellae underneath the fifth toe. Temporal region is covered with large tubercles widely separated by small scales. Postmentals are half the size of the gular or smaller. Rostral enters nostril.

Color pattern: Common color of dorsum light yellowish gray, with 4-5 dark and light cross bars, which extend on to tail. Ventral side is white. In general males are larger than females and have broader head (Baha EL Din, 2006).

1.3.1.1.3. *Tarentola mauritanica juliae* Joger, 1984

Synonymies: *T. m. mauritanica* Bons, 1959 (non Linnaeus, 1768)

Distribution: Distributed In the southwest Morocco, in the Moroccan high Atlas Mountains (on the coast region north to Essaouira); in south to the main ridge of anti Atlas (see figure 5).

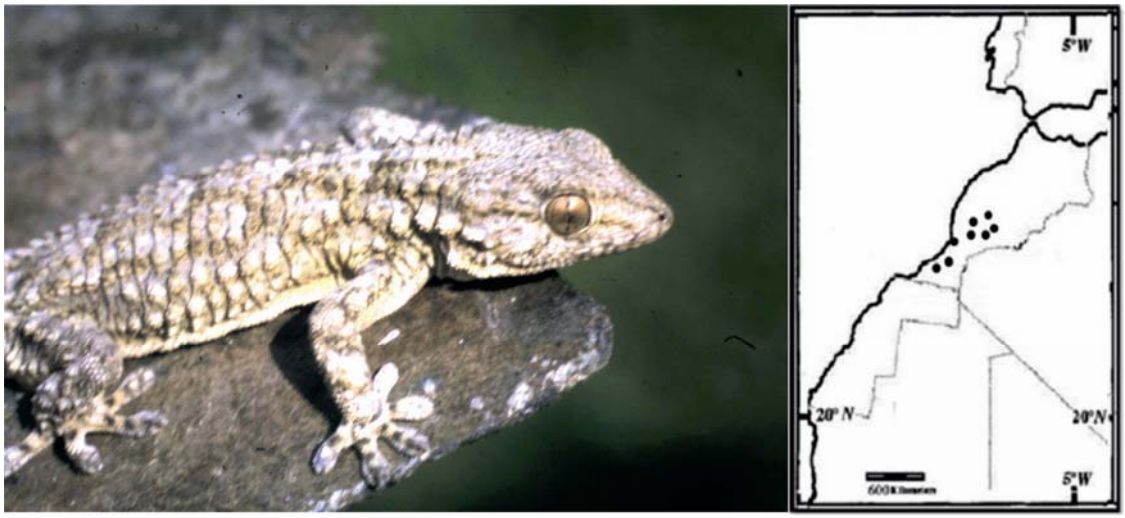

Figure 5. In the left photograph of an adult *Tarentola mauritanica juliae*, from Morocco. Source: photograph by U. Joger; and in the right side map shows the distribution range of this subspecies.

Diagnosis: Medium size lizard, SVL 54 mm; thin tail, 66 mm length. With shortly pointed head, males are larger than females, and with broader heads. Nostril in contact with rostral; 12-16 interorbital scales; gular scales count 28-40; eyes relatively large (eye diameter 3.6 mm). Dorsal region with star-shaped small and pointed tubercles, 14-15 longitudinal rows of dorsal tubercles, and 98-150 small scales around mid-body. A lack of enlarge tubercles on the border between dorsal and ventral scales. 17-21 lamellae and scales underneath the fifth toe.

Color pattern: Gray-brown dorsally, with 5-6 relatively thin, w-shaped branched dark transverse bars; Iris reddish (Joger, 1984a).

1.3.1.1.4. *Tarentola mauritanica pallida* Geniez et al, 1999

Distribution: It is distributed, from southwest Morocco to the Western Sahara (see figure 6).

Diagnosis: middle-size, adult animals up to 61mm SVL. Gular scales 32-45. Vertebral tubercles small and keeled; dorsal tubercles middle-sized, nearly flat, keeled, not bordered by a row of secondary tubercles; flank tubercles high, relatively large, keeled, each one with two small tubercles on either side and

Figure 6. In the left photograph of an adult *Tarentola mauritanica pallida*, from Dchira, Western Sahara, Source: Geniez et al, 1999 (photograph by M. Geniez); and in the right side map shows the distribution range of this subspecies

bordered by a row of secondary tubercles. Tubercles with one large central keel and several small secondary keels derived from the central keel. Rostral scales reaching nostril. Low numbers of subdigital lamellae, 17-19 underneath the fifth toe (Geniez et al, 1999).

Color pattern: Iris pinkish grey. Distinguishable from *T. m. mauritanica* and *T. m. juliae* by its pale, pinkish or yellowish general coloration (derived the name *pallida* from its pale color).

1.3.1.2. *Tarentola deserti* Boulenger, 1891

Common name: Desert wall gecko

Synonymies: *Tarentola mauritanica* Pasteur & Girot, 1960 (partim, non Linnaeus, 1758)

Distribution: It has a north Saharan range, from eastern and southeastern Morocco through Algeria to central and southern Tunisia (see figure 7). It is suspected to occur in northwestern Libya. It is found up to 1.300 m above sea level (Joger, 1984a).

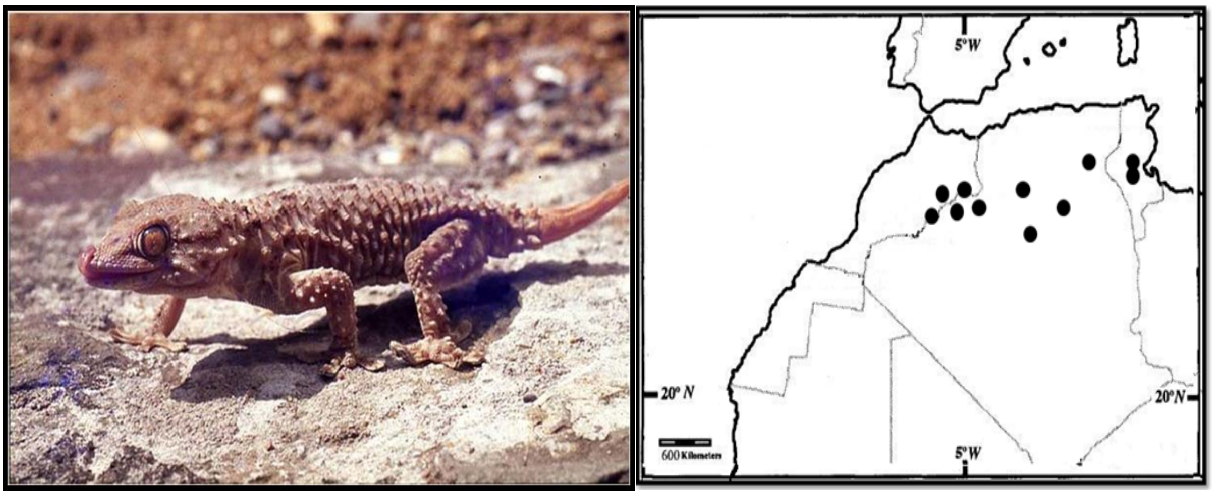

Figure 7. In the left photograph of *Tarentola deserti*. Source: photograph by U. Joger; and in the right side map shows the distribution range of this species

Diagnosis: Total length up to 190 mm; SVL males more than 100 mm, females 81 mm. With very flat and broad head in both sexes, very prominent tubercles; 13-15 interorbitals; nostrils not in contact with rostral; with 131-180 scales around midtrunk; dorsal tubercles prominent and pointed, with a sharp median keel and weak lateral ones, with rosette, except 1-2 median rows; dorsals clearly smaller than ventrals which are sharply delimited by a ventrolateral edge and fold. Gular scales count 45-59. With 21-24 lamellae and scales underneath the fifth toe.

Color pattern: Light pink, orange, beige to reddish dark brown, with pattern of 5-7 transversal bars which are often reduced to patches or lack altogether. Iris yellowish-ochre (Joger, 1984a).

1.3.1.3. *Tarentola boehmei* Joger, 1984

Common name: Morocco Wall Gecko

Synonymies: *T. ephippiata* Bons, 1959 (non O' Shaugnessy, 1875)

? *T. mauritanica deserti* Bons, 1959 (non Boulenger, 1891)

T. mauritanica Pasteur & Girot, 1960 (partim, non Linnaeus, 1758)

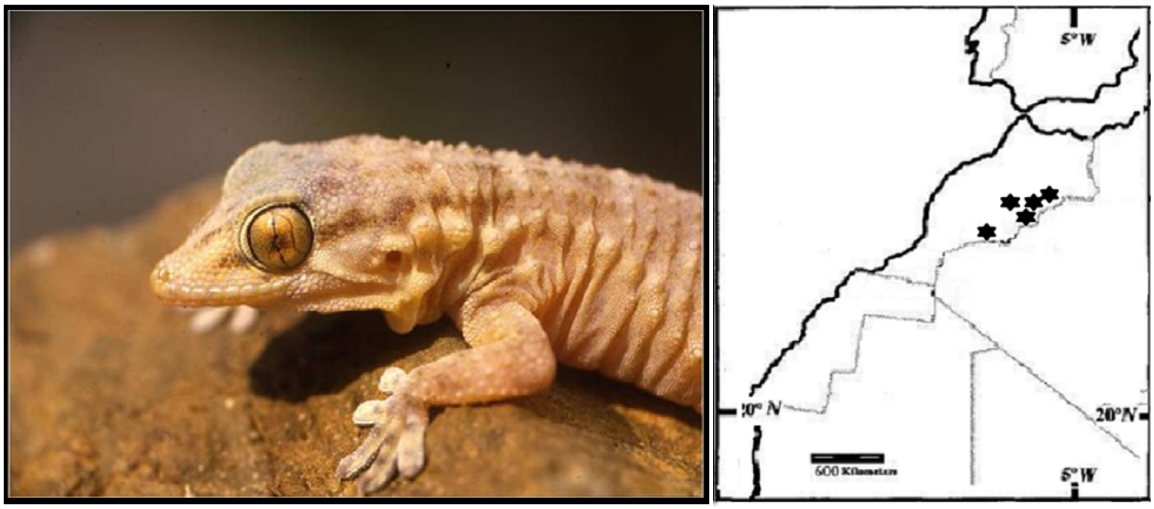

Figure 8. In the left photograph of an adult *Tarentola boehmei,* Morocco. Source: photograph by U. Joger; and in the right side map shows the distribution range of this species.

Distribution: It is an endemic to Morocco (see figure 8), distributed mainly between Tazzarine and Alnif, in South Morocco (Joger, 1984)

Diagnosis: Medium size lizard, SVL males 81.5 mm; females 73 mm. With narrow pointed head, short pointed snout (male head length 21.3 mm, head width 15.0 mm), nostril contact rostral, 15-17 interorbital scales; gular scales count 42-48; eyes relatively large (eye diameter 4.8 mm). Dorsal region with small scales and tubercles, dorsal region: low tubercles with stellate keels, rosette only around lateral tubercles; dorsal scales substantially smaller than ventrals, sharply delimited; a ventrolateral edge and fold; 133-177 scales around

midtrunk. Foreleg 26 mm, hindleg 36 mm. 21-23 lamellae and scales underneath the fifth toe (Joger, 1984a).

Color pattern: Light grey; with mid-dorsally a dark, ladder-shaped pattern; two dark zigzag stripes on each side which include a hexagonal field; the pattern can be reduced to interrupted ‘‘steps’’ of the ladder or even dark patches. Nape with four longitudinal streaks which dissolve into spots on the head; they also can be much reduced.

1.3.1.4. *Tarentola mindiae* Baha El Din, 1997

Common name: Qattara Gecko

Synonymies: *T. m.mauritanica* Loveridge, 1947 (part, specimen from Jialo, Libya)

T.m.mauritanica Marx, 1968 (part, specimen from Ain Shefa, Siwa)

Distribution: Distributed in northwest Egypt and northeast Libya (see figure 9). In Libya it is known from only one single specimen (BMNH1932.3.6.5) from Jialo oasis. This specimen was collected in 1932. According to Baha El Din, many other inland records of *T. mauritanica* in Cyrenaica probably refer to *T. mindiae*. In Egypt *T. mindiae* is known from Qattara Depression, Siwa Oasis and their surroundings (Baha El Din, 2006).

Figure 9. In the left photograph of an adult Qattara Gecko *Tarentola mindiae*, for Egypt. Source: photograph by Baha El Din; and in the right side map shows the distribution range of this species.

Diagnosis: Medium-sized and robustly built lizard, adult reaching up to 81 mm SVL. Covered with regular bands of protruding tubercles in back side, those on

dorsal surface of tail round and obtuse. Tubercles have a strong middle keel and a lot of lateral keels and are surrounded by rosettes of 5-8 medium-sized scales in ‘‘a horseshoe-like’’ shape. Tubercles are separated laterally from each other by 2-3 little scales. Tubercles on temporal region unclear and separated by subequal scales. There is one row of enlarged Postmentals that are 3-5 time larger than the gulars. Digits moderately dilated; there is an average of 16 lamellae underneath the fifth toe. Rostral excluded from the nostril.

Color pattern: Dorsum light- brown with 5-6 blackish bands across back between occiput and sacrum. A neck, two dark, near-parallel lines run on the snout from the rostral to the interorbital region. There are additional irregular dark streaks and marbling on top of head and on limbs. Venter gray-white, each scales with one or more very small dark spots. Iris is ochre (Baha El Din, 2006).

1.3.1.5. *Tarentola ephippiata* O’ Shaugnessy, 1875

Common name: Hoggar Gecko

Distribution: It is found in the southern half of the Sahara and North of tropical Africa (extended from Senegal to Northeast Sudan, see figure 10). From the four known subspecies, only *T. e. hoggarensis* live in Sahara, it is recorded in some mountains and rocky area in desert environments where is seems to be confined to *Acacia* trunks (Bons et al, 1996)

Four subspecies have been described from this species:

Diagnosis: Total length up to. 250 mm; SVL max. 100 mm (male 82.5 mm, female 79 mm); with a quite large and broad head (head length 27 mm, head width 18 mm, although not reaching the dimension of *Tarentola annularis*). The saddle is formed by a fusion of dark dorsolateral patches. 10-14 (most 11-13) interorbital scales; 8-10 supralabials, 7-8 infralabials. Between mental and gular scales 2 or 3 larger scales rows. No other *Tarentola* of this region shows this peculiarity 28-37 gulars. Dorsal tubercles rounded, smooth and flat or with a single keel, not much prominent, without rosettes; ventrals not much smaller than

dorsals, not sharply delimited. Very large scales, 68-98 around midbody. 16-25 lamellae and scales underneath the fifth toe.

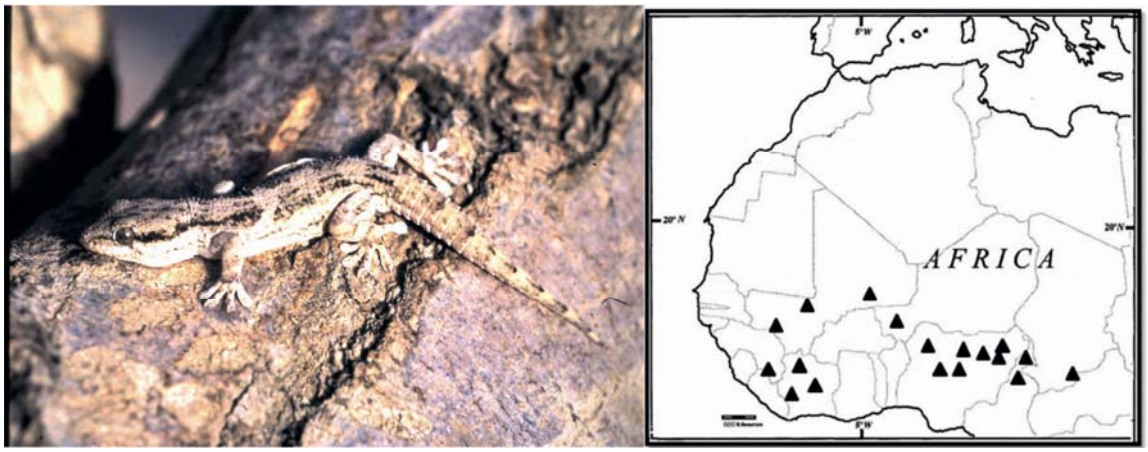

Figure 10. In the left photograph of an adult *Tarentola ephippiata.* Source: photograph by U. Joger; and in the right side map shows the distribution range of these subspecies: ▲ *T. e. ephippiata,* ● *T. e. hoggarensis,* ■ *T. e. senegambiae.*

Color pattern: Grayish-brown; contrasting dorsoloateral dark patches can fuse middorsally to a different degree forming w-shaped saddles or fuse laterally (forming a ladder); often a light middorsal stripe (Joger, 1984a).

1.3.1.5.1. *Tarentola ephippiata ephippiata* O' Shaugnessy, 1875

Distribution: It is ranging from Northern Ivory Coast, through Ghana, Togo, Benin, Southern part of Mali, Nigeria, Cameroon, Niger, to the Lake of Chad (Joger, 1984).

1.3.1.5.2. *Tarentola ephippiata hoggarensis* Werner, 1937

Synonymies: *T. delalandii* Angel, 1938 (non Dumeril & Bibron, 1836)

T. panousei Pasteur, 1959 (T. typical: Hamada du Dra)

T. neglecta Wake & Kluge, 1961 (non Strauch, 1895)

Distribution: Distributed from northern Niger, northern part of Mali, through southern Mauritania, Western Sahara until some Oases in southern Morocco (Joger, 1984).

1.3.1.5.3. *Tarentola ephippiata senegambiae* Joger, 1984

Distribution: Distributed throughout western and central Senegambia and extending eastward to reach Guinea-Bissau (Joger, 1984).

1.3.1.5.4. *Tarentola ephippiata nikolausi* Joger, 1984

Distribution: Only known from the coastal region of northern Sudanese Red Sea. Supposed, many samples of *T. ephippiata nikolausi* from Somalia are in reality related to *T. annularis* (Joger, 1984a).

1.3.1.6. *Tarentola parvicarinata* Joger, 1980

Common name: Sierra Leone wall gecko

Distribution: It is found in Mauritania (Mauritanian Adar) and extending southward over the hills in Ostsenegal and Westmali to Guinea, and an isolated population in Sierra Leone (see figure 11). Some population introduced anthropogenically probably follows the railway line Kayes-Dakar (Joger, 1984a).

Diagnosis: Relatively big in size, SVL up to 97 mm in males, 85 mm in females; complete original tail usually larger than head and body together. Have rough scales, with small star-shaped, keels tubercles, 103-184 small scales around

mid-body, normally 12 longitudinal dorsal tubercles (rarely 13 or 14). 34-54 gular scales; 21-25 scales and lamellae underneath the fifth toe.

Color pattern: Light brown or ochre-yellow in life animals, and mostly white in alcohol specimens (Joger, 1984a).

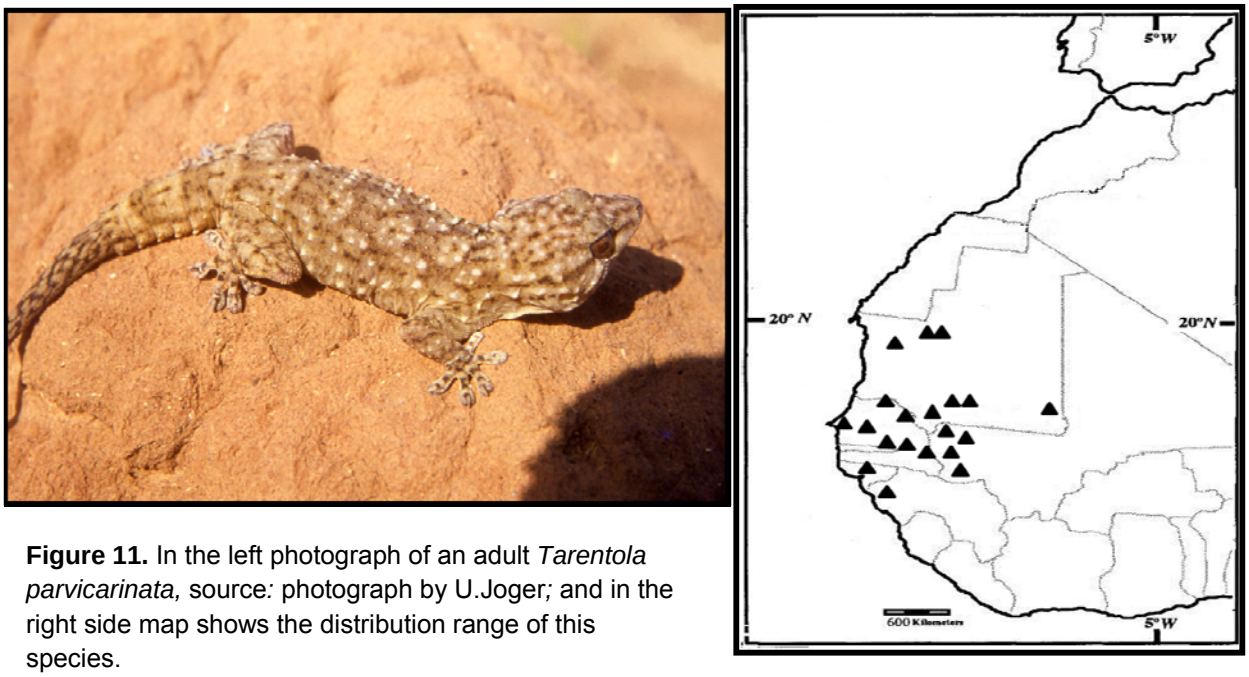

Figure 11. In the left photograph of an adult *Tarentola parvicarinata,* source*:* photograph by U.Joger*;* and in the right side map shows the distribution range of this species.

1.3.1.7. *Tarentola annularis* Geoffroy, 1809

Common name: House Gecko

Two subspecies have been described:

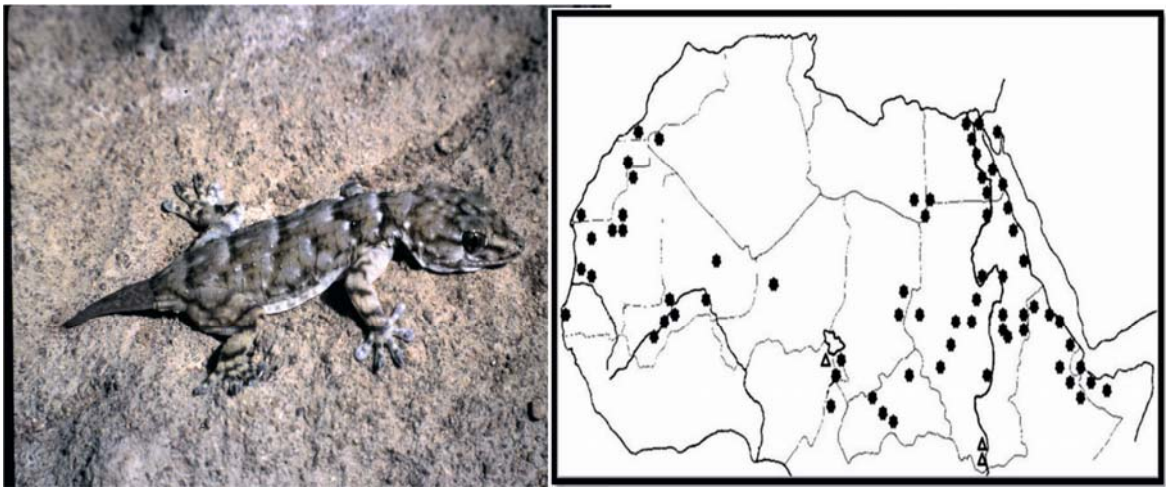

Figure 12. In the left photograph of an adult *Tarentola annularis annularis.* Source*:* photograph by U.Joger*;* and in the right side map shows the distribution range of these subspecies: ● *T. annularis annularis,* Δ *T. annularis relicta* .

1.3.7.1. *Tarentola annularis annularis* Geoffroy, 1809

Synonymies: *Gecko savignyi* Audouin, 1809 (T.typ: Egypt)

Gecko aegyptiacus Cuvier, 1829 (T.typ. restr. [Loveridge 1947]: Egypt)

Tarentola senegalensis Boulenger, 1885 (T.typ: Goree)

T. ephippiata Boulenger, 1895 (non O' Shaugnessy, 1875)

T. annularis quadraticauda Tornier, 1905 (T. typ.: Warabot, Somalia)

Distribution: *T. a. annularis* is distributed in a wide area cross Africa (see figure 12), it is found in disjunct areas between southwest Morocco and Algeria, extending over the western Sahara to Mauritania, to Niger, Mali, northern Cameroon, some rocky areas of Central African Republic, Chad, northern and central Sudan, to the north along the Nile to the Nile Delta and Sinai Peninsula (Egypt), Eritrea, Djibouti, Somalia, Libya (in the southeastern desert, Kufra Oasis), and Jebel Auenat (Joger, 1984).

Diagnosis: A robustly built lizard, male larger than female and have broader head. Reaching up to 140 mm SVL. Back and dorsal surface of tail covered with regular bands of low and smooth tubercles. Tubercles without obvious rosettes of medium-sized scales. Tubercles are separated laterally from each other by 6-7 small scales. There is an average of 27 lamellae underneath the fifth toe. Temporal region covered with large tubercles widely separated by small scales. Postmentals smaller than the gulars. Rostral enters nostril (Baha El Din, 2006).

Color pattern: General color of dorsum varies depending on dominant color of habitat and environmental factors, but commonly the color of dorsum ranges between dark brown-gray to light sandy-gray. Back with 4-5 dark and light crossbars and there are usually 4 distinctive white spots with dark borders on the scapular region (the white spots are commonly not very clear in juvenile animals, but become well developed and distinguish in adults). Tail with light and dark bands.

1.3.1.7.1. *Tarentola annularis relicta* Joger, 1984

Distribution: It is known from a limited area near Juba and Nimule in the South of Sudan (see figure 12), and Mora in North-West Cameroon (Joger, 1984).

Diagnosis: distinguishable from subspecies *T.n.annularis* by lacking the white scapular spots, and by repeatedly keeled scales and tubercles. And discernible from *T. parvicarinata* by higher number of scales, especially the toe lamellae.

Color pattern: Uniform color (staining) without white and black tubercles.

1.3.1.8. *Tarentola neglecta* Strauch, 1895

Common name: Algerian wall gecko

Two subspecies have been described from the species:

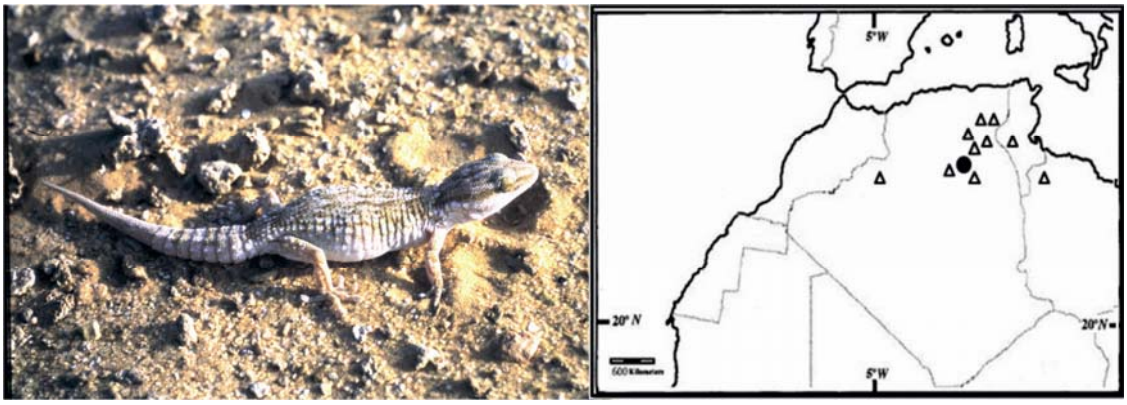

Figure 13. In the left photograph of an adult *Tarentola neglecta.* Source*:* photograph by U.Joger; and in the right side map shows the distribution range of these subspecies, Δ *T. neglecta neglecta,* ● *T. negleca geyri.*

1.3.1.8.1. *Tarentola neglecta neglecta* Strauch, 1895

Synonymies: *T. angusticeps* Strauch, 1895 (T. typical: Batna)

Distribution: Distributed South of the Sahara-Atlas (see figure 13), from Algeria, Tunisia to West Libya (northern Sahara) (Joger, 1984).

Diagnosis: Relatively small lizard, maximum SVL 59 mm male, 51 mm female. Full tail 10-15% longer than SVL. Abdominal scales slightly larger than dorsal scales, 72-98 small scales around mid-body; slim head, 10-12 interorbital scales; 28-39 (mostly under 36) gular scales; 13-15 scales and lamellae underneath the fifth toe (up to toe base).

Color pattern: Basic color from ochre-yellow to reddish-brown, with thin dark lines (typically lines are drawing the head with four parallel lines on the snout, and two converging, which are often connected together as V-shape. On dorsal region normally 6 to 7 narrow saddle spots between the neck and middle sacral (Joger, 1984a).

1.3.1.8.2. *Tarentola neglecta geyri* Joger, 1984

Distribution: It occurs in South Algeria in central Sahara, from the southwestern edge of the great eastern Erg to the foothills of the Hoggar Mountains (see figure 13). The exact delimitation of the distribution area is still unclear (Joger, 1984).

Diagnosis: In pattern and proportions of the same as subspecies *T. n. neglecta*, but they differ in, ventral scales slightly of the same size as dorsal scales, and possess 38-40 gular scales, 15-18 scales and lamellae underneath the fifth toe (Joger, 1984a).

Color pattern: the same color as *T. n. neglecta***.**

1.4. Area of study

1.4.1. Historical evolution of the Libyan plateau and North Africa.

In this section, we will give briefly overview about the geology of North Africa in general and in particular Libya. And try to explain, how Libya is created with these land forms.

The upper mantel (Lithosphere), in which the continents are embedded, is in constant motion. According to the theory of Plate tectonic, mountains are created when two continental plates collide, and rock layers are folded and vaulted.

In the Carboniferous (about 350 Mya), there were only two continents on Earth. These were Gondwana in the south and Laursia in the north. The supercontinent Pangaea, which existed from around 230 Mya, was the result of a clash and the unification of the two super-continents (Gondwana and Laursia). Through ever constant energy from the interior of the Earth, Pangaea eventually broke apart again. Then the old Laurussia broke in North America and Eurasia, and the former Gondwana fragmented to Africa, South America, India, Antarctica and Australia. Present-day Africa is the central remnant of the ancient southern supercontinent Gondwanaland. The fracturing of this massive supercontinent took place during the Jurassic period (middle segment of the Mesozoic era) between 195 – 135 Mya. Plate tectonic is the responsible force for this cleave. Today the African plate and the African continent are occupying about one-fifth of Earth´s land surface and its continents, respectively. Africa thus stores a significant volume of scientific information needed to better understand how the Earth works, how it has evolved, and how it might far in the future (De Wit, 2006). The Oceanic portion of the plate records 180 My of continuous Oceanic Lithosphere formation while the continent´s oldest rocks recorded date about more than 4.0 billion years old, in central Africa. Africa is at least 3.8 billion years old (in its present form or joined with other continents, as it was in the past). Structurally, Africa is consisting of five cartons, with well preserved sequences and Lithosphere sections, the anatomy of which provide profound insights into

key concepts of geologic and biologic co-evolution, and the origin of Earth's first continents.

African sits on the African plate, a section of earth´s crust bounded by mid-oceanic ridges in the Atlantic and Indian Oceans. The entire plate is creeping slowly toward the northwest at a rate of about 2 cm per year.

The African plate is unique in the global perspective in several ways:

1- The African plate is nearly stationary, and in an embryonic state of dividing into two new plates. African plate is spreading or moving outward in all directions, and therefore Africa is growing in size. Geologists say that, in the next 50 My East Africa will split off from the rest of the continent, along the East Africa rift, which extends about 6.400 km from the Red Sea in the north to Mozanambique in the south.

2- The bimodal topography of most continents can be related to processes across compressional plate tectonic margins, this is not so for Africa. Africa is surrounded by more than 90% by extensional plate margins, and the state of stress across its upper continental crust is predominantly extensional. However, Africa is host to some of the world's greatest elevated regions (southern and East African highlands), and of the world´s fastest rising continental blocks (Rwenzori mountains).

On the basis of previously described continental drift, the plate tectonics, the origin of the Libyan area was as below:

The Libyan area was from the Precambrian to Permian under intensive undulations and folded of the earth´s crust. Due to the enormous stress of the rock curls and basins formed within this area. One of the first wave formations of the North African plate was the cause of the Caledonian orogeny, although it took in Europe its beginning, but indirectly contributed to geological processes on the African plate. The grave consequences of this movement were multiple fractures and cleavages in the Libyan area. One of the main ditches is the Hun ditch

(located in the North of the country) and also, the Hercynian orogeny that followed took up the African plate.

The Carboniferous resulted in further ties and pelvic structures in Libya. In the east of the country is the big Sirte basin, the special feature here is that, the underground water can be found in sandstone fossil (fossil-powered water).

In the north-west lies Hombra basin. It is the starting point for a series of dry valley systems, here is the cultivated areas or even favorable habitat surrounded by the Saharan desert, extending over hundreds of kilometers and. This includes high density of population or human settlements.

In the south-west the Murzug basin is situated (called also Fezzan basin), where the major Libyan Oases lie. Moreover, here lies the Acacus Mountains, they have a height of about 800 – 1000 m and have exotic shapes. On top of the mountains is a flat surface consisting of a rocky desert called Al Hamada El Hamra. The forthcoming sandstone is under constant tectonic pressure and highly stressed, leading to the formation of cracks and towers of rock. The sandstone which makes up the mountains, contributes to the formation of Great Sandy Desert (formation of dunes).

The emergence of the Acacus Mountains in Murzuq basin can be declared as follow:

In the Paleozoic, the supercontinent Gondwanaland and the Primordial Sea (Tethys Sea) constituted, North Africa was covered by a primeval ocean. The sea level was correspondingly high at this time. Over the years, pitched in on the huge amounts of sediment from the North Africa plate, this resulted in the Mesozoic finally in pressure; this pressure pushed the interior great sediments and rocks from the high elevation to the out. The deposited sediments were than no longer below but above sea level. Over the time, the sea retreated, the area was drained, and the sediment deposited, and represented a single mountain. Through processes of Aeolian and fluvial erosion a water network was formed in the Pluvial, the rock has been continually eroded. Since the mountain consists

only of soft sandstone, nature had an easy time eroding the rocks. It caused major Wadis in the interior of the mountain (Burchards & Sanftleben, 2005).

In the Pleistocene epoch 1.6 million – 11.000 years ago, the Sahara was subjected to humid and then to dry and arid phases, spreading the Sahara Desert into adjacent forests and green areas. About 5.000 – 6.000 years ago in the post glacial period of our modern epoch (Holocene), a further succession of dry and humid stages further promoted desertification in the Sahara. Libyan Sahara Desert, as mentioned above consists in large part of Gravel desert (Serir, about 10%), rocky desert (Hamada, about 70%), and in the pelvic region is divided into sandy desert (about 20%). The dune fields are arranged in the direction of the prevailing trade winds.

El Jabal Al Akhdar and Jabal Nefusa mountains are both results of these pressures, which have emerged on the raising events of the Paleozoic. The former African plate at that time basically just gave up to the mountains of Jabal Nefusa (Abdulsamad et al, 2008). The Jabal Nefusa bears a slight incursion into the south, with some volcanic eruptions and basalt areas.
Today's mainland north of the Jabal Nefusa is actually a marine sedimentation, after the sea has receded. It reaches to an altitude of about 800 m. Similar to the Atlas Mountains; it provides a natural barrier separating inland and coastal area. But the two mountains have a different origin. The Atlas Mountains are much younger, dating from the Tertiary; the Jabal Nefusa comes from the carbon and is therefore older.

Tertiary and Quaternary volcanic activity, which mainly occurs at the fault zones and the elevation zones, produced any quantity of basalt, and all types of volcanoes. The basement occurs only at very high mountains to the prominent surface. This can be in the Tibesti Mountains in the northern portion of Chad, and extends into southern Libya recognized easily; it represents the highest mountains in the Sahara with very rugged terrain and shows numerous volcanic craters (the highest peak is Emi Koussi, with 3415 m altitude). Tibesti is one of the most isolated regions of the earth.

In the central region of Libya, the coastal region south of Sirte, range desert sometimes up almost into the sea. No mountains here are the climatic barrier. Flat salt plains stretch along the coast and go over into the inland to flat limestone.

1.4.2. Physical setting of the study area

1.4.2.1. Location of Libya

Libya is situated in northern Africa, between latitudes 20 to 34° N and 10° to 25° E. With an area of 1.759.549 sq km, Libya is one of Africa´s largest countries; it is fourth in size among the countries of Africa and fifteenth among the countries of the world (McMorris, 1979). More than 90% of the country area is desert or semi desert, Libyan Desert is part of the African Sahara, and largely consists of barren rocky and sandy desert. Libya is bounded by the Mediterranean Sea to the North, with a coastline of nearly 1.800 km. The country borders, Tunisia in the north-west (459 km), Algeria lies to the west (982 km), Chad, Niger, and Sudan to the south (1.055 km, 354 km, and 383 km respectively), Egypt lies to the east (1.115 km) (CIA, 2004).

1.4.2.2. Libyan regions and their landforms

In general Libya consists of barren plains in the north, contrarily plateaus and depressions in the south (see Fig.14); the Mediterranean coast lands and the Sahara desert are the most prominent natural features. Although there are several highlands, but no true mountains exist, except the Tibesti Mountains in southern desert near the Chad-Libya border (McMorris, 1979).

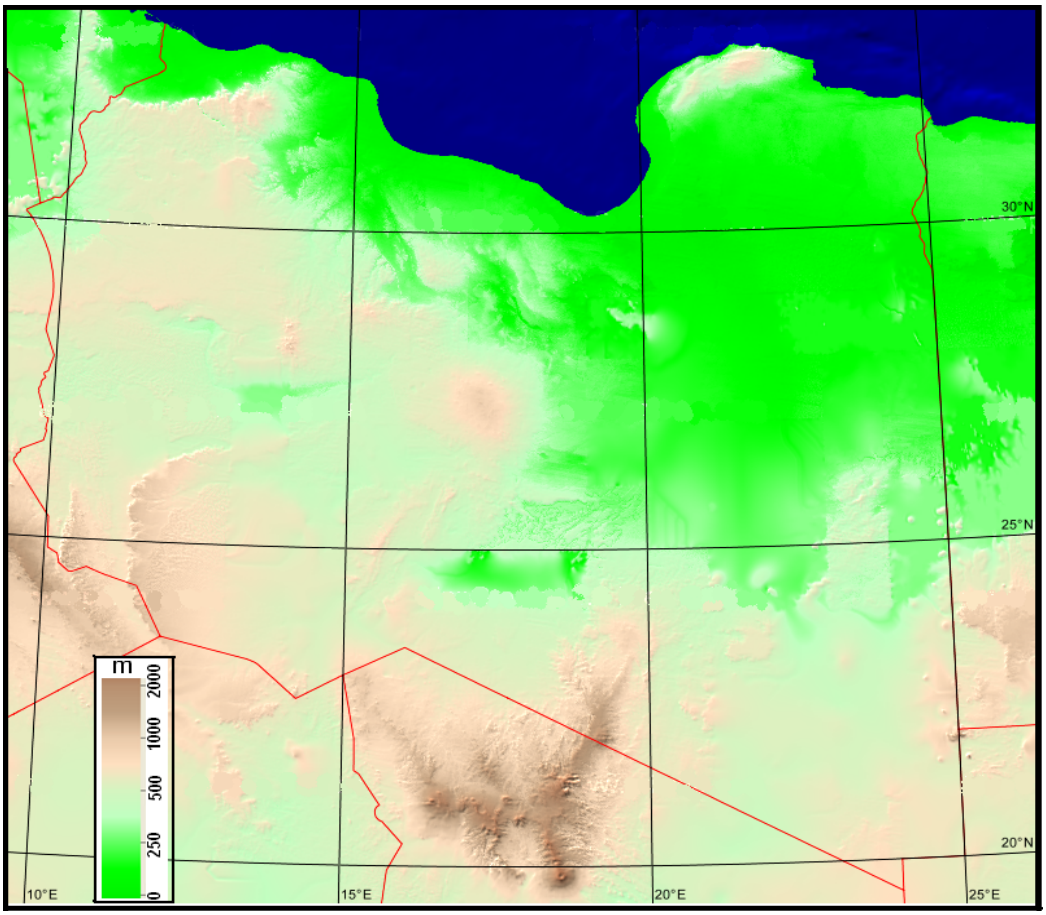

Figure 14. The map shows the topography of Libya. (Created with Map Creator program)

The dominant features of the northern coastal zone are the low-lying areas; the lowest point is Sebkhat Ghuzayil, 47 m below sea-level (CIA, 2004). The Mediterranean coastal zone of Libya extends from the Tunisian border in the west, to the Egyptian border in the east, over 1.900 km in length and ranging between 15 –100 km in width (Ben-Mahmoud et al, 2000). The main contrast is between narrow enclaves of fertile lowlands along the Mediterranean coast, and the vast expanse of arid rocky plains and sand dunes to the south (Nelson, 1979). In the northern portion of the country, coastal plain includes coastal lowlands (Jifara Plain, Sirte Plain, Banghizh Plain) as well as Lagoons, Sebkhas, Salty marshes, Swamps, and coastal sand dunes. Coastal lowlands are separated here from each other, by pre-desert zone and backed by plateaus with steep (north facing) scarps.

Libya consists of three main regions, some of which are divided into sub regions:

1- Tripolitania (North-West region)

The north-west region, Tripolitania has characteristics similar to those of nearby Tunisia, Algeria, and Morocco. With these states it makes a supranational region called Maghreb. Tripolitania rises from the narrow coastal plain in a series of steps until it reaches the Jafara plain and the Jabal Nafusah plateau. Along the shore of Tripolitania for more than 300 km, coastal Oases alternate with sandy areas and Lagoons. Inland from these lies the Jafara Plain, a triangular area of about 15.000 sq km. About 120 km to the south (inland) the plain terminates in an escarpment, the land here rises to form the Nafusah mountains, with elevation between 600 up to 1000 meter above sea level, these form the northern edge of the Tripolitania Plateau (Pesce, 1968; Barich et al, 2006).

Nafusah Mountains (Western mountain) lie on the boundary between the Jafara coastal plain, to the north, and the Tripolitania Plateau to the south. the strata of the Tripolitania Plateau slope downwards to the south and tilt upwards towards the north creating the highest portion of the plateau as the Nafusah mountains which rise to over 960 meters. The plateau ends abruptly on the north with an escarpment which has up to 350 meters of topographic prominence (Asketell & Ghellali, 1991; El Zouki, 1980; Megeris et al, 1980). A series of deep drain Valleys (Wadi´s) north toward the Jefara cut into the escarpment. To the south, Jabel Nafusah grades southward to an extensive plateau with stone desert, called Al Hamada El Hamra, which persist at heights of about 500 m (Pallas, 1980).

2- Cyrenaica (North-East region)

The north-eastern region of the country, in Cyrenaica there are fewer coastal Oases, along the coast the precipice of an arid plateau reaches to the sea. The

Marj Plain (the lowland area) forms a crescent about 210 km long between Benghazi and Darnah and extends inland a maximum of 50 km (McMorris, 1979). Behind the Marj Plain, the terrain rises abruptly to form Jabel Al Akhdar (Green mountain), it´s so called because of its vegetation (its leafy cover of pine, juniper, cypress, and wild olive). Jabel Al Akhdar is formed of a limestone (Paleogene limestone), with maximum elevation reaching to 900 meters (Griffiths, 1972). From Jabel al Akhdar, Cyrenaica extends southward across a barren grazing belt that gives way to the Sahara Desert, which extends still farther southwest across the Chadian frontier. Same elevation is gained further to the east by shallow gradation of Sirt Gulf hinterland. In the east the low table-shaped elevation surround the gravel areas (Serir desert), ample in place and in parts covered by extensive basalt slabs towards the south. The volcanoes rise to 800m above sea level in El Sawda Mountain and up to 1,200 m in the Haruj Es Sawda Mountain (Kanter, 1976).

3- Libyan Sahara Desert (Southern region, Fezzan)

In general about one-third of the Earth surface is desert, deserts are mainly found around the tropical of Cancer and tropical of Capricorn in the northern and the southern hemisphere respectively. In common definition of desert is a region that receives less than 250 mm of rain per year on average.

African Sahara (The greatest desert, see figure 15) is a part of world deserts; Sahara with 9 million sq km is the largest desert on Earth. It covers ca 25% of Africa and takes an area larger than the continent of Europe, with extent over 6000 km, from the Atlantic Ocean in the west up to the Red Sea in the east. Including parts of the Mediterranean coasts, to the south it is delimited by the Sahel, a belt of semi-arid tropical savanna that comprises the northern region of central and western Sub-Saharan Africa.

Libyan southern region (known as Fezzan) is a part of African Sahara, and has desert climate which is very harsh and dry. In Libyan Desert regions, the three largest Oases are Al Kufrah, Ghat, and Ghudamis.

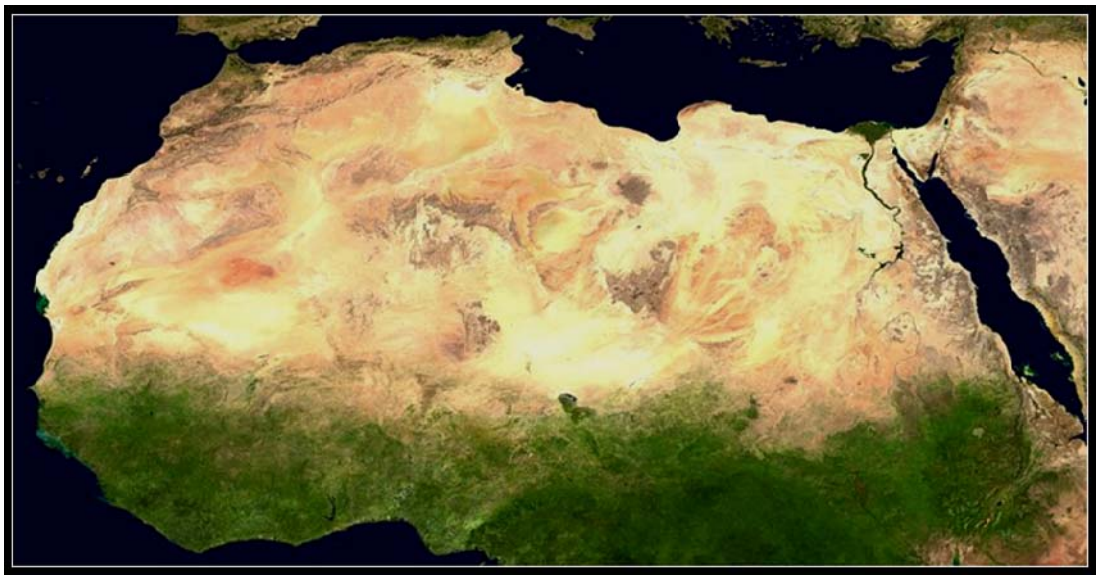

Figure 15. A satellite image of the African Sahara desert. Source: NASA.

Largest Oases are Al Kufrah, Ghat, and Ghudamis. Here, underground water resources are tapped by means of shallow wells (Burchads & Sanftleben, 2005). Wadi Kiam is Libya´s only permanently flowing river, it is only about 2 km in length, flowing from its spring source in the western province down to a lagoon reservoir close to the Seashore. All other Wadis run dry during the hot weather, but flash floods are common during the rainy season. In southern Libya, the ecoregion is made up of two isolated mountain areas. In the central part of Sahara desert, Tibesti mountains (Acacus mountains), lying halfway between Lake of Chad and Gulf of Sirt, the large part of these mountains area is found in the northern portion of Chad, and extend into southern Libya; they consist of several inactive volcanoes, with the highest peak reaching 3.415 m (McGinley, 2007). Tibesti Mountains are prominent and very rugged slopes, dip gently north and eastward, the board valley stretches northward from Ghat Oases and great sand seas of Murzug and Ubari, which are separated from the Serir Tibesti by the Nubian-Post-Tassilian outcrops of Jabel Ben-Ghnema and Jabel El-Gussa (Pesce, 1968). In the southeastern region, and access to the vicinity of El Kufra, low hill ranges rise to some 700 m, small oases, and near the southern border;

Jabel Uwainat which located along the intersection of southeastern Libya, southwestern Egypt, and northwestern Sudan. Jabel Uwainat includes peaks reaching elevation of 1.934 m (Kanter, 1967).

1.4.2.3. Climate

Upon location, Libya has a sub tropical climate. Libya's climate is mainly influenced by the interaction between the Mediterranean Sea and Sahara desert, so air masses of either continental or maritime origin effect climate. The coastal belt has a Mediterranean climate, with average temperatures in Tripoli ranging from 30°C in the summer to 8°C in the winter. The coast area receiving more efficient precipitation against the dry, vast area occupied by the Sahara desert. The mountains have very important effects on the climate, they act as strong barriers which block the further passage of air masses associated with a different pattern of precipitation on the windward and leeward side either (Domroes & Gongbing, 1988: 26). In Libya, there are no mountain ranges stretching either from west to east or from north to south, therefore the Saharan effect extend northwards to the Mediterranean coast (gulf of Suirt). Jabel Naffusah and Jabel El Akhdar in the northern part of Libya have local effects on climate (precipitation and temperature); high mountains and plateau are colder than low elevations. The influence of the air lifting effect of mountain peaks and ranges on winds that pass over them, as air reaches a mountain barrier, it rises and produces clouds and precipitation on the windward side of the mountain. After it crosses the crest, it descends the downwind side of the mountain (Scott, 2001). Rainfall is mostly during the winter months, it varies on average from 0 mm in the southern regions to 600 mm in the coastal regions annually (Martyn, 1992). Coastal cities can be humid, with levels of humidity as high as 80% in Tripolitania and Cyrenaica. The mountain regions experience more rainfall, particularly during the winter and early spring. Summer here is cooler than on the coastal plain. The south part of the country has a desert climate with daytime winter temperature ranging between 15 and 20°C, falling below zero at night. During summer months the temperatures reach to over 50 °C, the highest temperature in the world was

recorded in Libya on the 13th of September 1922 in El Azizia close to Tripoli; it was 58 °C (Burchads & Sanftleben, 2005).

1.5. Previous studies

Although scarce studies concerned herpetofauna of Libya, the available data about previous herpetological studies in Libya show, that all of them yielded/ or resulted in the addition of new records to the known herpetofaunal species (Werner, 1909; Boulenger, 1914; Zavattari, 1930; Scortecci, 1935a, b, c, 1937a, b; Schnurrenberger, 1958; Kramer & Schnurrenberger, 1963; Joger, 1984a, b; Schleich, 1987; Schleich, 1989; Sindaco, 1995; Schleich et al, 1996; Laurent et al, 1997; Frynta et al, 2000; Joger, 2003; Wilms, 2004; Agrasar et al, 2004; Harris et al, 2004a, b; Ibrahim et al, 2005; Ibrahim & Ineich, 2005; Ibrahim, 2008; Kapli et al, 2008; Joger et al, 2008; Perera & Harris, 2008; Harris et al, 2009).

Most of previous activities in Libya were concerned with snake fauna, and concentrated in northern portion of the country (Tripolitania and Cyrenaica).

For example, Zavattari (1930), in his study (Erpetologia della Cirenaica) described *Tarentola mauritanica* from Cyrenaica.

In (1935 and 1937) Scortecci identified a leptotyphlopid (*Leptotyphlops macrorhynchus*) and toad (*Bufo regularis*) from Ghat in the extreme south-western Libya.
Kramer and Schnurrenberger (1963) reported 18 species of snakes from Libya; most species were from northern regions.

Joger (1984), described three species of *Tarentola* in Libya: 1) *Tarentola mauritanica fascicularis* from the specimens collected by Loveridge in 1947 from Ain Zeyanah, 20 km south of Banghazi (Cyrenaica, Libya), and housed in ZFMK-Bonn under number 35631, distributed along Mediterranean coast. 2) *Tarentola*

neglecta neglecta in west Libya. 3) *Tarentola annularis annularis* in El Kufra Oases and Jabel Auenat in the extreme southeastern Libya.

Schleich et al (1996), in his book Amphibians and Reptiles of North Africa, reported 50 species of amphibians and reptiles from Libya, the authors reported four species of genus *Tarentola*: 1) *Tarentola mauritanica fascicularis* from the North Libya, along Mediterranean shore; 2) *Tarentola deserti* from the north-west Libya (not far away from Libyan Tunisian borders); 3) *Tarentola* neglecta, from northwest Libya; 4) and *Tarentola annularis* from El Koufra, in the extreme southeastern Libya.

Frynta et al (2000) recorded 25 reptiles and two amphibians from 30 different sites in the country of which only one toad and 11 reptiles from south regions. He recorded *Tarentola mauritanica* in Cyrenaica.

Joger (2003), in his work on Reptiles and amphibians of southern Tunisia, explains that the *Tarentola* from Djerba island in Tunisia and western Libya, also, still need formal description; they have a mixture of morphological characters, they could be assigned to *Tarentola mauritanica*, but electrophoretically they seem to be closer with *Tarentola deserti,* they might be subspecies of *Tarentola deserti;* but in the same time, *Tarentola m. fascicularis* (from Libya and Egypt) should be considered, as well.

Harris et al (2004), in his work investigating the phylogenetic relationship within *Tarentola mauritanica* group*,* the analysis included samples from Morocco, Algeria, Tunisia , and only four samples from Libya, they were described as *Tarentola mauritanica fascicularis*, collected from Cyrenaica (specimens Tm22 from Maquis [near Banghazi], Tm23 from Om Arazam, Tm26 from Tobruk, Tm21 from Libya/Egypt borders). They found the *Tarentola m. fascicularis* from Libya is genetically divergent from *Tarentola m. mauritanica*, with at least 8% uncorrected p-distance for 12S & 16S rRNA partial gene sequences.

Ibrahim et al (2005, studied the Lizard *Chalcides ocellatus* from Cyrenaica (Banghazi).

Ibrahim (2008), in his work [Contribution to the herpetology of southern Libya], studied the herpetofauna of southwestern Libya (Fezzan), the study carried out during 2005-2006, in this expedition two amphibian and 18 reptile species were recorded. Of these 16 reptile species are reported for the first time and one lizard was identified as *Tarentola mauritanica* from Sabha city (Fezzan).

Kapli et al (2008), studied Lizards from genus *Mesalina* in North Africa, included two species in Libya one from Tripolitania (*M. olivieri*) and other from Cyrenaica (*M. guttulata*).

Joger et al (2008), two blind snakes were collected from Bu Gheilan, in the western mountain (Libya), the specimens were identified as *Ramphotyphlops braminus*, these was the first record of this species in Libya, and the second in North Africa (the first, was recorded in Egypt by: Baha El Din,1996).

Harris et al. (2009), the authors investigated the relationship between *Tarentola mauritanica* from SW Italy islands (Lampedusa and Conigli), and North African *Tarentola,* they used the Libyan previous samples (Tm21, Tm22, Tm23, and Tm26) from Harris et al (2004). Their result shows that, the Conigli and Lampedusa specimens separated in two clades, one approximately identical to a specimen from Libya (Tm21, which is genetically described as *Tarentola m. fascicularis*), and the other distinct from all currently sampled specimens. They explain that, the island specimens are more closely related to those from Libya, and could have reached the islands from North Africa, either via natural rafting or anthropogenic introduction.

Considering the above herpetological studies in Libya, it is clear that, all of them lack precise information on the genus *Tarentola* in the country (their geographical distribution and diversity). All previous studies were based on few specimens, from limited area. There is still need to extensive sampling to describe correctly patterns of genetic diversity for several reasons. First, to know the classification and distribution of *Tarentola* in Libya. Second, to determine the relationships between this genus in Libya, and other related *Tarentola* species in the other regions. And finally, Libya is a biogeographically complex area with two differentiated bioclimatic regions (Mediterranean climate and Sahara climate); these make it a country with a variety of environmental factors (different habitats).

1.6. Aims of work

Among the North African countries, Morocco, Algeria, Tunisia, and Egypt; the herpetofauna of these countries is very well studied, a large amount of studies were carried out. This is also true for the genus *Tarentola,* where many species and subspecies are recognized (e.g., Boulenger, 1891; Anderson, 1898; Bons, 1958; Marx, 1968; Blanc, 1978, 1979; Joger, 1984a; Blanc and Ineich, 1985; Nouira & Blanc, 1986; Joger & Bischoff, 1989; Le Berre, 1989; Salvador, 1996; Bons and Geniez, 1996; Schleich et al, 1996; Willand, 1997; Saleh, 1997; Joger et al, 1998; Nouira & Blanc, 1993; Joger, 2003; Baha El Din, 2006,) . On the contrary studies about this genus in Libya are sparse, however the genus *Tarentola* has been poorly investigated, and very few species were assessed. Libya is still the least studied when compared to adjacent countries in North Africa, Libya represents a gap of information about the genus *Tarentola* in North Africa. Special attention in this study was laid on Libya, because it is located in the same geographical region (North Africa), and the knowledge of our biodiversity resources is still far from complete, they are also not very well studied.

The present work is considered as one of the primary studies that are concerned with the evolution and geographical distribution of the genus *Tarentola* in Libya.

The main objectives of this study are:

- To unravel the phylogeography and evolutionary history ''evolution and biodiversity in space and time'' of the genus *Tarentola* in Libya.
- To determine the relationships between different forms of *Tarentola* in Libya, and other *Tarentola* species and subspecies in the North Africa.
- And try to fill a knowledge gap on the biogeography of this genus in North Africa.

➢ **Assumptions**

- *Tarentola mauritanica fascicularis* probably is found in a narrow band along the Mediterranean coast across northern Libya.
- *Tarentola mindiae* probably is found in northern Cyrenaica.
- Many inland records of *Tarentola mauritanica* in Cyrenaica probably refer to *Tarentola mindiae*.
- *Tarentola neglecta* probably is found in Fezzan, southwest Libya.
- *Tarentola deserti* probably is found in northwest Libya.
- Morphologically similar Operational Taxonomic units (OTUs) can be genetically different.

➢ **Special questions:**

- Is there a chance of finding new taxa from genus *Tarentola* in Libya?
- Does new taxon *Tarentola. sp* from south-central Tunisia extends eastward to north-west Libya?

02 MORPHOLOGICAL STUDY

2.1. Introduction

Variation in the structure is a main source of characters and character states in taxonomic and systematic studies (Michaux, 1989; Lauder, 1990). The reasons of geographic variation in populations can be both historical, involving phylogenetic relationships and the influence of historical vicariance events and allopatric development, and ecological, with adaptation to local conditions influencing characters (Thorpe, 1987). Morphological similarity has created considerable taxonomic uncertainly among North African *Tarentola*, new species and subspecies of gecko *Tarentola* were recently described from North Africa (Joger, 1984a; Baha El Din, 1997).

Several external morphological traits have been used to investigate and identify the relationships between species. Variation in a specific morphological trait is usually accompanied by variation in other morphological, physiological or behavioral traits, both within species and between species (Emerson & Arnold, 1989).

The aim of present work is to review the geographical variation of North African *Tarentola*, and to pay special attention to the patterns of their geographical differentiation through North Africa, to establish whether there is adequate shape (morphological) variation between the forms to separate them into different species and subspecies, and to summarize these differences and show that the population of Libya might present new taxa, and to describe any resulting new species or subspecies.

As Libyan *Tarentola* are geographically located between the population of north-east Africa (Egypt) and north-west Africa (Tunisia, Algeria and Morocco), Libya provides the link in the west-east transition. Only little attention has been paid to study the *Tarentola* of Libya, this study is one of the first studies that are paying

attention in this lizard in Libya. The morphometric analysis of *Tarentola* of Libya in this study therefore provides an essential link to understand the characteristics, biogeography and spread of this gecko in North Africa. In this study, we perform a morphometric analysis to compare between different species and subspecies of genus *Tarentola* in North Africa with new collection of *Tarentola* from Libya. Morphological data were recorded from available material of *Tarentola* from Libya as well as from museum materials. Morphological characters relating to scalation, color pattern, and body proportion have been examined. Multivariate statistics were used to discriminate among different forms of gecko *Tarentola.*

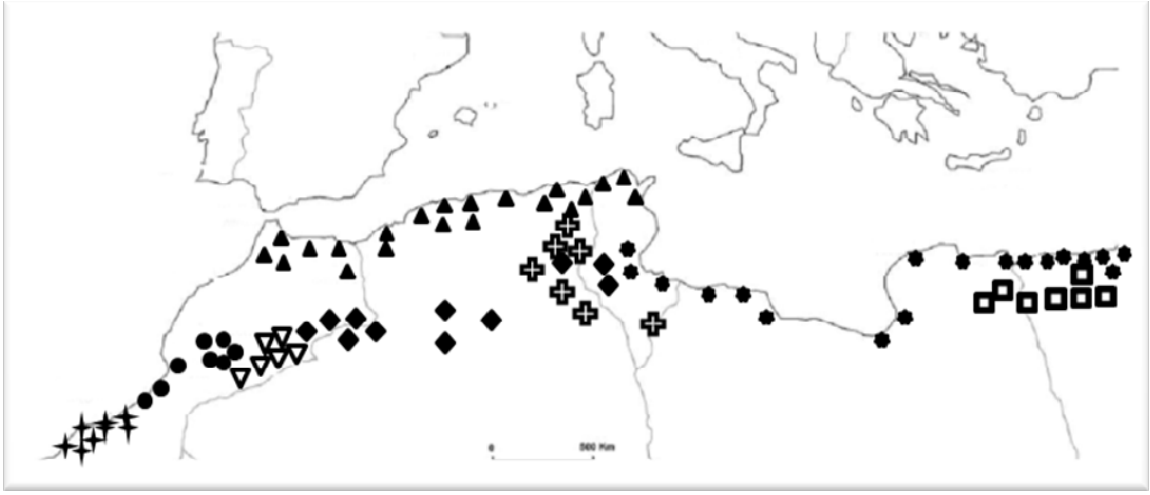

Figure16. Distribution map of genus *Tarentola* in North Africa(taxonomy as understood before the present work), ▲*T. m. mauritanica*; ● *T. m. fascicularis*; ● *T. m. juliae*; ✚*T. m. pallida;* ▼ *T. boehmei;* ◆ *T. deserti* ; ✤ *T. neglecta;* ■ *T. mindiae.* Source modified after: Joger, 1984 a,b; Geniez et al, 1999; Baha EL Din, 2006.

The previously known data reveal an unexplained gap in the distribution of genus*Tarentola* in North Africa. As this area from North Africa is quite poorly investigated from a zoological point of view, the gap is probably an artifact due to poor sampling. The gap shown in distribution map (figure 16), between the population of north-east Africa and north-west Africa is not discussed in depth in the literature.

Indeed, this study of the morphological characters in the genus *Tarentola* revealed several morphological differences between the samples from Libya and other samples from the rest of its distribution range in North Africa. *Tarentola* of Libya differ in many respects from those of other parts of North Africa.

2.2. Material and Methods

A total of 466 specimens, representing different formes of the genus *Tarentola* have been studied. To quantify morphological variation among the studied species and subspecies, the voucher specimens were collected through field work from various localities in Libya; additional specimens were kindly provided from various collections.

2.2.1. Preserved material

In total 149 voucher specimens from various collections were studied, these specimens were collected from different localities in Europe and Africa. The museum animals are almost always preserved in denatured ethanol 70-85%; they were removed for examination from their vessels and put back after examination. We have studied these specimens to compare with our specimens from Libya to clarify the relationships between them. These specimens were borrowed from the following museum collections:

ZFMK- Zoologisches Forschungsinstitut Museum Koenig, Bonn, Germany.

SHNM-BS- Staatliches Naturhistorisches Museum, Braunschweig, Germany.

MNHN- Muséum National d′ Histoire Naturelle, Paris, France.

SMF- Senckenberg Forschungsmuseum Frankfurt/M, Frankfurt, Germany.

HLMD- Hessisches Landesmuseum Darmstadt, Darmstadt, Germany.

ZIBU- Zoology Institute Banghazi University, Banghazi, Libya.

BEV- University of Montpellier, Montpellier, France.

2.2.2. Field work

The first trip to Libya was between May and June 2007, and covered the northern part of the country, the study site covers an area of about 175,000 km^2, from Itwellia in the extreme northwest of Tripolitania up to Tobruk in the extreme

northeast of Cyrenaica, 299 specimens were collected in this trip, from 22 different localities (12 localities in Tripolitania, and 10 localities in Cyrenaica), these specimens represent different local forms of the genus *Tarentola*.

The second trip to Libya was between September and November 2008, and concentrated in the southern regions of the country, the work carried out in the south-west of the country (called also Fezzan, or Sahara desert), the collection area covers at least 21,000 km^2, from Bin Ulid in the north up to Ghat and Elperkat in the extreme south-west part of the country.18 *Tarentola* specimens were collected in this trip, the specimens were collected from 13 different localities in Libyan Sahara desert, and represent different forms of the genus *Tarentola*.

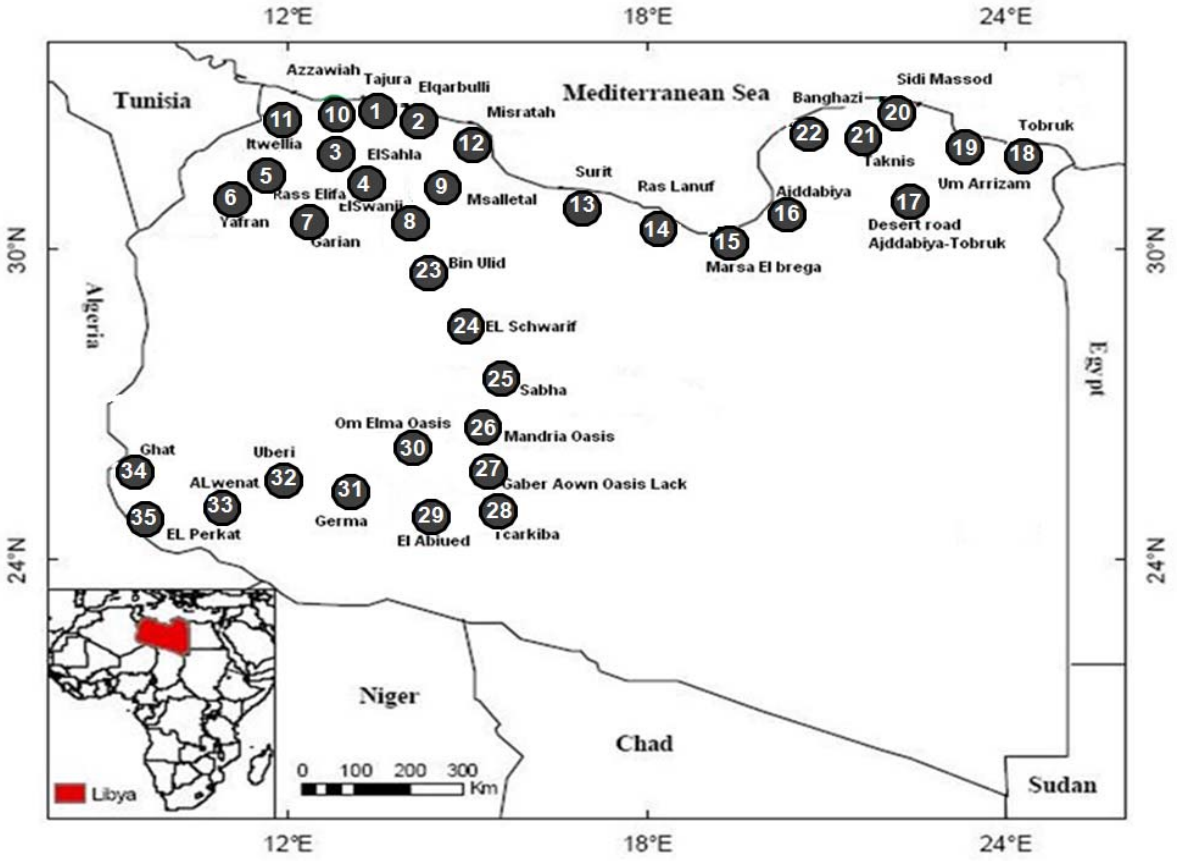

Figure17. Map of Libya showing main study sites: 1)Tajura; 2)El Qarbulli; 3)El Sahla; 4)El Swanii; 5)Rass Elifa; 6)Yafran; 7)Garian; 8)Tarhunah; 9)Msalleta; 10)Azzawiah; 11)Itwellia; 12)Misratah; 13)Suirt; 14)Rass Lanuf; 15)Marsa El Brega; 16)Ajddabiya; 17)Desert road Ajddabiya-Tobruk; 18)Tobruk; 19)Um Arizam; 20)Sidi Massod; 21)Taknis; 22)Banghazi; 23)Bin Ulid; 24)El Schwarif; 25)Sabha; 26)Mandria Oasis; 27)Gaber Aown Oasis Lack; 28)Tcarkiba; 29)El Abiued; 30)Om Elma Oasis; 31)Germa; 32)Uberi; 33)Alwenat; 34)Ghat; 35)El Perkat.

From the field work 2007 and 2008, in total 317 voucher specimens were collected, I have covered the area of about ¾ of the country. Figure 17 shows the map of Libya with study sites.

Field work sites were selected to represent different type of habitats (diversity of biotopes), including gravel desert or firm ground (‘‘*reg’’*, which makes up a large fraction of the desert in Libya), temperate and montane steppe (mountainous limestone plateaus), sand deserts (*erg*) and rocky plateaus (hammada), valleys (‘‘*oued’’*, dry river beds), palm oasis; searches for geckos *Tarentola* were undertaken around all these areas, (see figures 59, 60, 61, and 62). The animals were captured from valleys under bridges, from abandoned ruins of buildings, buildings under construction, from drains under roads, also in the gaps between the cement barriers in mountain roads, from olive trees under the crust and palm trees, too. The average search time for each field day was about 8 to 10 man-hours. The survey was made during the day and night; the lizards were collected on sunny, warm days when lizards were assumed to be active, at preferred daily body temperatures. They were collected manually by hand and with help of torch lights and head lamps at night. Other sampling techniques were used: turning rocks over; climbing trees and search at trees branches, and also under the crust of their trunks and branches. The Global Positioning System (GPS) was used to provide information about reliable positioning, navigation, and the elevation of different collection sites (see table 2).

2.2.3. Preparation of voucher specimens for morphological study

Once collected, *Tarentola* specimens were taken notes on their life-coloration. The specimens were then euthanized by injection with chlorobutanol solution (solution composed of just a little chlorobutanol crystals dissolved in water and little amount of absolute ethanol), about 5 ml in the lizard’s abdominal region; or freezing. After that the animal dies. Immediately tissue samples were taken for molecular study. Vouchers were fixed by injection with absolute ethanol in the body cavity and muscles, then immersion of the whole animal in a bowl containing 90-100% ethanol (absolute ethanol), left in the bowl from 1-2 hours,

and subsequently put into plastic jars with 75% ethanol to preserve. The voucher specimens were housed in the herpetological collection of Staatliches Naturhistorisches Museum Braunschweig (SHNM-BS) Germany.

Table 2: Lists of all collect sites in which the animals have been collected in Libya

Locality	Coordinates	Elevation
Azzawiah	N: 32° 39' 01.03'' E:12° 45' 31.18''	76 m
Itwellia	N: 32° 34' 07.64'' E:11° 59' 02.89''	57 m
Tajura	N: 32° 48' 16.17'' E:13° 30' 49.82''	37 m
El Qarbulli	N: 32° 45' 02.66'' E:13° 37' 22.25''	43 m
El Sahla	N: 32° 39' 58.84'' E:12° 55' 26.97''	80 m
Rass Elifa	N: 32° 10' 27.58'' E:12° 27' 08.79''	213 m
Yafran	N: 31° 56' 31.97'' E:12° 15' 20.21''	668 m
Garian	N: 32° 09' 54.62'' E:13° 00' 35.78''	717 m
El Swanii	N: 32° 37' 22.77'' E:13° 02' 20.07''	92 m
Tarhunah	N: 32° 25' 47.05'' E:13° 38' 28.25''	408 m
Msalleta	N: 32° 32' 54.28'' E:14° 00' 44.37''	208 m
Misratah	N: 32° 18' 37.01'' E:15° 12' 20.32''	2 m
Suirt	N: 31° 10' 49.67'' E:16° 44' 29.09''	30 m
Ras Lanuf	N: 30° 29' 56.12'' E:18° 31' 26.01''	13 m
Marsa El Brega	N: 30° 23' 14.45'' E:19° 36' 58.67''	29 m
Um Arizam	N: 32° 31' 30.59'' E:23° 00' 05.51''	78 m
Tobruk	N: 32° 01' 02.40'' E:23° 57' 50.37''	127 m
Desert road Ajddabiya-Tobruk	N: 31° 10' 40.45'' E:22° 22' 37.96''	131 m

Locality	Coordinates	Elevation
Ajddabiya	N: 30° 45' 40.94'' E:20° 12' 25.10''	1 m
Banghazi	N: 32° 24' 01.76'' E:20° 28' 14.98''	70 m
Taknis	N: 32° 28' 46.97'' E:21° 07' 45.80''	435 m
Sidi Massod	N: 32° 50' 16.11'' E:21° 47' 36.17''	361 m
Bin Ulid	N: 31° 45' 03.92'' E:13° 59' 27.83''	262 m
EL Schwarif	N: 29° 58'43.32'' E: 14° 15' 35.74''	345 m
Sabha	N: 26° 59' 25.43'' E:14° 25' 09.22''	430 m
Gaber-Aown Oasis Lake	N: 26° 30. 370'' E: 013° 21. 378''	467 m
Om Elma Oasis	N: 26° 43. 282'' E: 013° 22. 047''	460 m
Mandria Oasis	N: 26° 45. 308'' E: 013° 19. 827°	465 m
Tcarkiba	N: 26° 33. 924'' E: 013° 15. 350''	460 m
El Abiued	N: 26° 35. 380'' E: 013° 04. 084''	462 m
Germa	N: 25° 47. 829'' E: 010° 33. 529''	458 m
Uberi	N: 26° 33. 467'' E: 013° 15. 154''	449 m
Al Wenat (Acacus mountains)	N: 25° 47. 566'' E: 010° 32. 404''	710 m
Ghat	N: 24° 48. 547'' E: 010° 09. 038''	677 m
El Perkat	N: 24° 47. 182'' E: 010° 11. 767''	693 m

2.2.4. Characters studied

A range of external morphological measurements relating to body proportions, scalation, and color patterns were taken from each specimen, whenever possible. All measurements were made multiple times until two or three consecutive readings were in agreement.

2.2.4.1. Biometric characters or morphometric characters

The following linear measurement points on the body were taken from each specimen, whenever possible. All linear measurements were taken with a digital caliper (measurement range: 0mm – 150mm, input-unit: 0,01mm, accuracy: 0,03mm, repeatability: 0,01mm), by the author to avoid inter-observer variability; used abbreviations and designations from Joger (1984a) are:

- Snout-vent length (SVL), calculated from snout tip to anterior end of cloaca in (mm).
- Tail length (TL), calculated from anterior end of cloaca to tip of tail in (mm), ‘‘only from original tails, tail measurements from individuals with regenerated or broken tails were not included’’.

- Head length (HL), the distance on mid-dorsal line between the tip of the snout and the line connecting the rear tips of the mandibles in (mm).
- Head width (HW), the distance at the widest part of the head in (mm).
- Head height (HH), measured as: perpendicular to body longitudinal axis at eye level in (mm).

- Forelimb length (FLL), from the axillar ring to the end of the fourth finger in (mm).
- Hindlimb length (HLL), from the groin ring to the end of the fourth toe in (mm).
- Eye diameter (ED), the longest diameter of the visible part of the eye in (mm).
- FHLL, distance between forelimb and hindlimb in (mm),

- (HDL), length of fourth toe, counted from their point of attachment near the third toe up to the end of toe in (mm), not including claw.
- (HDW), maximum width of the fourth toe in (mm).
- (ASL), distance from the front edge of eye up to snout tip in (mm).
- (IOB), distance between the eyes, counted from the closest point in (mm).
- (AOL), distance from the posterior edge of the eye to the ear opening in (mm).
- (MOL), distance from the middle point of the imaginary line between ear openings up to the mental in (mm), see figure 20.

2.2.4.2. Scalation characters

The following scalation features on the body were taken from each specimen, whenever possible; methods of recording some of head and limbs scalation are demonstrated in figures 18 and 19, these characters were taken by binocular microscope; used abbreviations and designations from Joger (1984a) are:

- 1^{st} toe, the number of scales and lamellae underneath the first toe, counted up to an imaginary line between the toes.
- 4^{th} toe, the number of scales and lamellae underneath the fourth toe, counted up to an imaginary line between the toes.
- 5^{th} toe, the number of scales and lamellae underneath the fifth toe, counted up to an imaginary line between the toes.
- 5^{th} toe base, the number of scales and lamellae underneath the fifth toe, counted up to toe base.
- Dorsal-Ventral (DV) enlarged tubercles between ventral and dorsal scales; (+) present, (-) not present.
- VS, ventral scales, the number of ventral scales, counted usually at mid-body in transverse row.
- Cr, the number of scales above the eye
- GS, the number of gular scales, counted as the number of scales from mental to the middle-point of an imaginary line between the ears.

- IOA, the number of scales between the eyes, counted from the closest point.
- BT, body scales, the number of scales around the middle body (without ventral scales)
- MS, mental scales, the number of scales which in contact with the mental.
- NK, nostril contact, with (+) rostral in contact with nostril, and (-) refers to the absence of a contact.
- Sublabialia, the number of scales for one side starting from the angle of the mouth to the middle of lower jaw, except mental.
- Supralabialia, the number of scales for one side starting from the angle of the mouth to the middle of upper jaw, except rostral.
- G, sex, (m) refers to male, and (f) refers to female.
- DT, the number of dorsal tubercles (tubercles = larger scales), in a transverse row at the body's center (tubercle row, fusing with another row, is counted as ½).
- DT (g/k), dorsal tubercles, with (g) the dorsal tubercles is smooth, and with (k) keeled.
- DT (s/m), dorsal tubercles, with (s) the dorsal tubercles is simply keeled, and with (m) bearing multiple keels.

2.2.4.3. Coloration

Coloration or color pattern, color of dorsal and presence or absence of transversal bars were recorded from live animals and also from alcohol preserved animals.

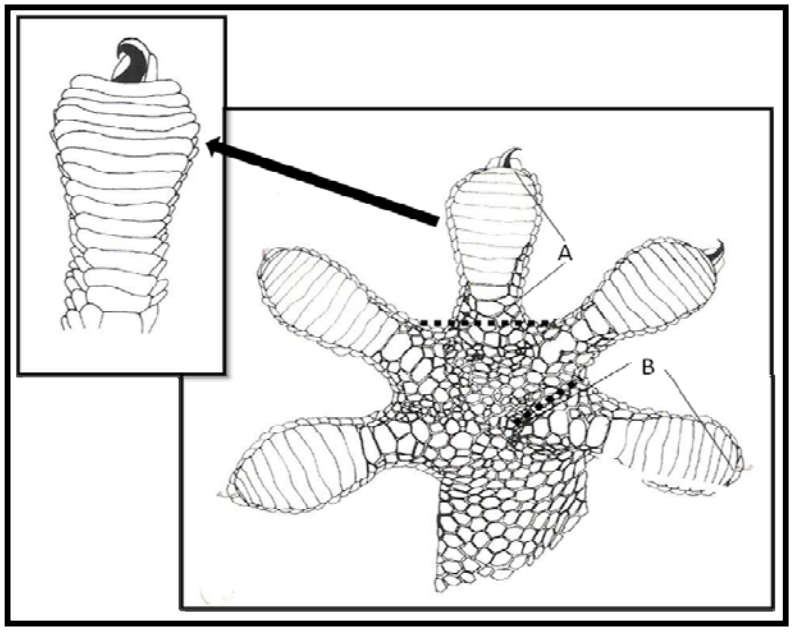

Figure 18. Shows underside of gecko *Tarentola* foot, explains the scales and lamellae counting method. (A): shows the starting and ending points in counting scales, at the 3rd toe, it is the same method used in 1st and 4th toe. (B) Shows the starting and ending points in the counting scales and lamellae to toe base, at the 5th toe. (Source: modified after Joger, 1984a).

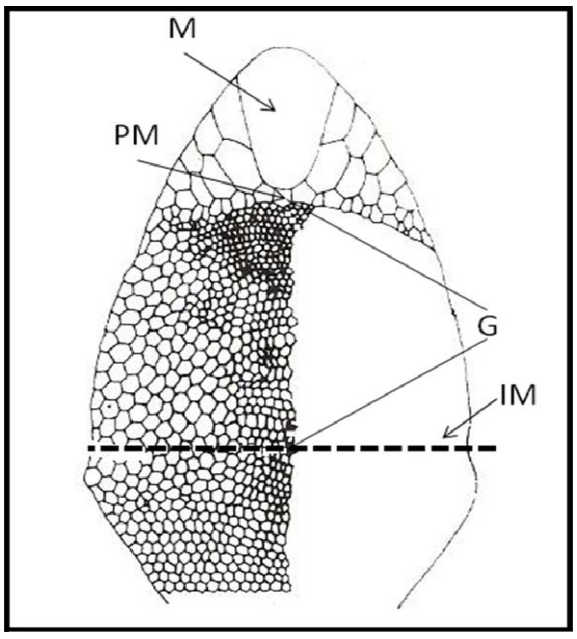

Figure 19. Ventral view of *Tarentola* head shows, (IM): The imaginary connection line between the ear openings, it is the starting point in the counting of gular scales; G: scales between mental and IM; PM: postmental; M: mental. (Source: modified after Joger, 1984a).

2.2.5. Statistical procedures

2.2.5.1. Preparation of the data

2.2.5.1.1. Separation of sexes

Significant sexual dimorphism in morphological characters has been observed in several species of reptiles (Cox & Alder, 2007). In this study, preliminary investigations indicated sexual dimorphism within operational taxonomic units (OTUs) for several traits. To avoid any confusing effects of sexual dimorphism females and males were treated separately.

2.2.5.1.2. Preliminary selection of operational taxonomic units

When analyzing patterns of geographic variation, it is necessary to discriminate between taxonomically relevant variation due to geographic disparities, and taxonomically irrelevant within locality variation. The specimens should be grouped into geographic samples, generally referred to as OTUs. Before performing further analysis (multivariate analysis), it is essential to determine the characters which are significantly variable among OTUs. Thus specimens must be assigned to preliminary groups prior to analysis.

In this study, preliminary OTUs (definition of groups) were initially defined on the basis of molecular data (see Figure 34, 12SrRNA tree, presented in the molecular phylogenetic part of this study), for the specimens from which we have their DNA sequences. For the specimens from which DNA sequences were not available (most of the museums specimens), we used geographic proximity to the OTUs defined by DNA and statistical tests (T-test and Mann-Whitney test) to determine the OTUs, see Table 6 and 7; in this case, we compared between two populations, one from which we have a DNA sequence, and another one from which we do not have a DNA sequence. We compared those using morphological characters, when two specimens are not significantly different; we assign them into the same OTU. To avoid assigning multiple members of different OTUs to the same group, these initial clusters were based on a subset

of specimens, belonging to geographically restricted groups. Groupings used in this study are detailed in the results.

2.2.5.1.3. Defining significantly variable characters

After specimens were assigned to initial groups, characters showing significant between group variations were statistically defined. A one-way ANOVA was utilized to determine whether there was significant between group variations for each character, see Table 8 and 9. A small number of characters showed very low levels of within group variation and it was necessary to check the distribution of values visually. Checked characters which did not show significant between group variations at the 0.05 level were rejected.

2.2.5.1.4. Preparation of biometric characters

True morphometric values or lengths were transformed into the non-dimensional ratios (Relative length), by dividing all lengths by SVL or HL, it is necessary to transform the measured values (absolute values) into relative lengths, to remove the effect of size on morphological variables, to be used in further analysis.

Head measurements were adjusted based on HL, and other body measurements were adjusted based on SVL. Non-metric (scalation) characters were not size-corrected.

2.2.5.1.5. Data checking and estimation of missing data

The entire data were carefully checked prior to analysis to ensure accuracy. Morphometric values were plotted against the appropriate co-variate (HL or SVL), and any data points which deviated significantly from the trend were confirmed using the original data sheets. Also meristic characters which deviated significantly from within group trends were checked against the original recordings.

2.2.5.2 Statistical analysis

Statistical analyses used in the study of external morphological characters are based on relative similarity or dissimilarity of populations with many characters considered simultaneously without a prior weighting (Jardine & Sibson, 1971; Sneath & Sokal 1973). We have extensively analyzed the relationships among populations of *Tarentola*, based on multivariate morphometric external characters, from existing museum and newly collected material from Libya. The data were described and analyzed by using IBM SPSS Statistic, version 18, and StatSoft, Inc. (2007), STATISTICA (data analysis software system), version 9, these programs including several methods for analysis and test. Several methods of statistics analysis were used:

2.2.5.2.1. Descriptive statistics method

This method concentrates on organization and presentation of data, describing the statements that have been obtained, and description by standard metrics; e.g. comprising arithmetic mean, standard deviation, maximum and minimum. These were used as an estimator of the intrinsic population variability; the results of all these analyses are detailed in the section of results.

2.2.5.2.2. Indicative statistics method

These are tools to test hypotheses using statistical tests, by analysis, interpretation and evaluation of results and drawn conclusions, according to the laws of certain statistics.

2.2.5.2.2.1. Univariate statistics

Using statistics analysis, to recognize the differences between two populations, e.g. T-test, U-test (Mann-Whitney test); and one-way ANOVA (comparisons of several populations), the results of all these analyses are detailed in the section of results.

A one-way ANOVA (single classification) was generated with SPSS statistical program. ANOVA was carried out separately for males and females; where significant differences were found, they were termed significant at $p < 0.05$ and highly significant at $p < 0.01$ for multiple comparisons among means.

2.2.5.2.2.2. Multivariate statistics

Applications of multivariate analysis in ecology and systematics were used for more than 50 years (for example, for the six-year period from 1983 to 1988, James & McCulloch found 514 applications in seven journals). In the last decades this technique was used intensively in biology to investigate the relationships between variables, and determine which variable distinguishes between two or more groups (James & McCulloch, 1990).

Multivariate analyses of community data are used to summarize redundancy, reduce noise, elucidate relationships, and identify outliers; their analyses serve to relate communities to other kinds of data. Results from these kinds of analyses serve to improve our understanding of the relationship between different variables (Beck et al, 1982). Classification and ordination are two types of multivariate analysis. Classification basically involves grouping entities together in clusters; ordination primary endeavors to represent sample and /or species relationships as faithfully as possible in a low-dimensional space. The end result is a graph, usually two dimensional, in which similar species are close to each other and dissimilar entities are far apart. Here we used to investigate the population systematics of *Tarentola* in North-Africa by two kinds of this technique.

1- Linear Discriminant Function Analysis (LDFA)

LDFA can be considered as a descriptive version of multivariate analysis of variance for two or more groups, and the idea is to find linear combinations of variables that separate the groups. LDFA can be used to summarize the results of an experiment; it is used in systematics most often as an exploratory ordination procedure (James & McCulloch, 1990). It is also a classification technique, mainly used to determine which variables discriminate between two or more naturally occurring groups. To clarify, a biologist could record different characteristics of similar types (closely related species), and then perform a LDFA to determine the set of characteristics that allows for the best discrimination between the species.

Previous to analysis, mensural characters (morphometric characters) were used in their transformed state (Rel-length); other characters (scalation characters) were used in original state (unchanged). A number of LDFA were carried out on subsets of the full dataset for each sex separately and the result used to unite groups or aid in the grouping of non aligned individuals. These are detailed in the section of results.

2- Principle Component Analysis (PCA)

PCA is an ordination technique (a kind of factor analysis); it has been widely used in all areas of ecology and systematics. It is a data reduction technique which can be used to identify the underlying components or factors that explain the correlations among a set of variables. Thus, it is possible to utilize a smaller set of measures (the factors) to explain a large portion of the total variance that explained the entire original variable, the method is based on maximization of the variance of linear combinations of variables; therefore data with several variables can be presented effectively on a two- or three-dimensional graph that uses the components as axes (James & McCulloch, 1990; Geber & Finn, 2005).

Prior to analysis, mensural characters (morphometric characters) were used in their transformed state, other characters (scalation characters) were used unchanged, and then all characters were standardized to zero mean and unit standard deviation (standardize the data by subtracting the mean and dividing by standard deviation). Thus, the centroid of the whole data set is zero, so different variables which measure in different units can be compared.

To test and improve upon the initial OTUs used to select significant variable characters, a number of PCAs were undertaken on subsets of the full dataset for each sex separately and the result used to combine groups or aid in the grouping of non aligned individuals. These are detailed in the section of results.

2.3. Results

Preliminary OTUs were selected based on a combination of phylogeny (Figure 34, 12SrRNA tree) and geographic proximity (as declared previously, in the part of material and methods), the initial selected groups are shown in table 3 and figure 20.

Table.3: Initial groups used to define characters variation, and their sample size (N)

mtDNA Clades	Group. Nr	Preliminary group	Distribution	N (males)	N (females)	Sum M&F
Clade H	1	*T. sp*-complex-Libya	Tripolitania-NW Libya	37	104	141
Subclade G1	3	*T. sp*-sister group Sabha	Suirt	1	3	4
Clade F	4	*T. deserti*-Libya	Libya	19	54	73
Subclade D1	5	*T. sp*-Ras Lanuf	Ras Lanuf-Cyrenaica	2	5	7
Subclade D2	6	*T. sp-sister* gr. Ras Lanuf	Cyrenaica	4	11	15
Clade C	7	*T. m. fascicularis*-Libya	Cyrenaica	3	12	15
Subclade B1	8	*T. neglecta*-South Libya	South-West desert	1	2	3
Subclade G2	10	*T. sp*-Sabha	Libyan Sahara desert	5	3	8
Clade A	13	*T. mauritanica*-Morocco	Morocco	9	9	18
___	14	*T. mauritanica* -Tripolitania	Libya (without precise locality)	3	5	8
___	16	*T. m. juliae*-Morocco	Morocco	15	15	30
__	17	*T. boehmei*-Morocco	Morocco	5	8	13
__	18	*T. mauritanica*-Tunisia	Tunisia	12	10	22
Clade E	19	*T. sp*-Tunisia	Tunisia	9	6	15
__	20	*T. mauritanica*-Algeria	Algeria	4	5	9
Clade F	21	*T. deserti*-North Africa	Algeria-Tunisia	14	10	24
Clade C	22	*T. m. fascicularis*	Egypt	2	2	4

- Note: The missing numbers were united with another numbers (for example: 2 with 1; 9, 11 with 10).

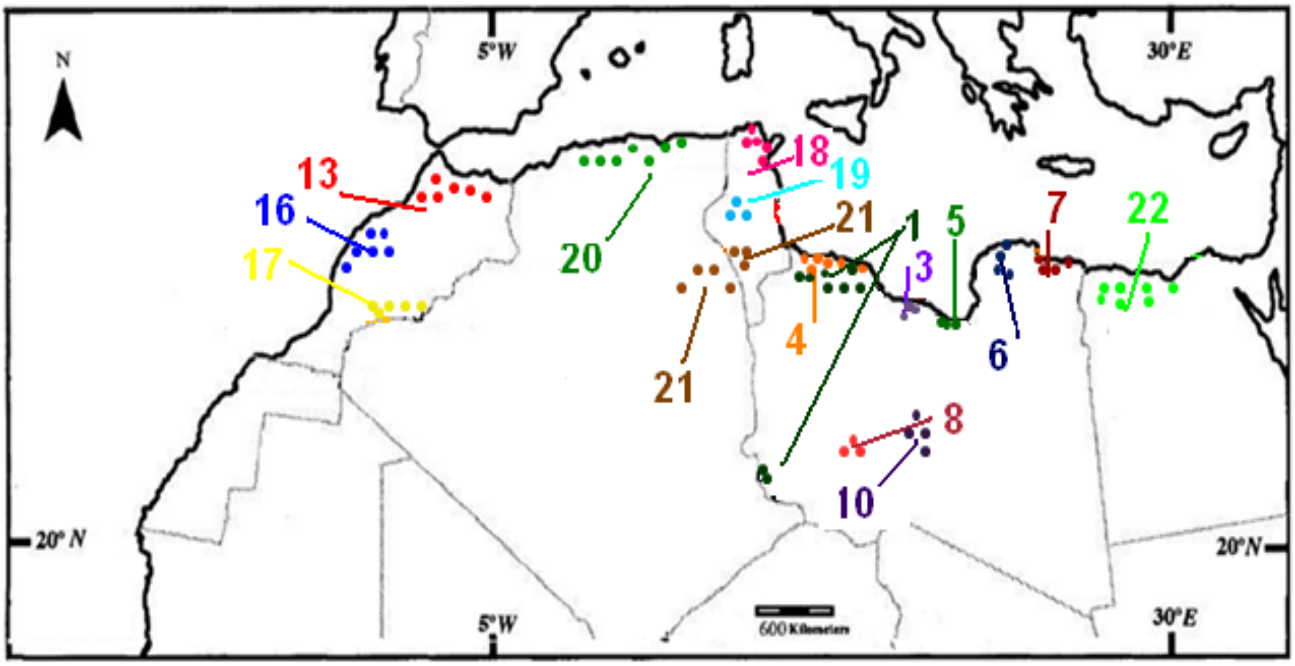

Figure 20: Map showing the groupings defined in table 3

Mean values, standard deviation of each morphometric and meristic character of *Tarentola* sample was computed (see tables 4 and 5). The investigated *Tarentola* sampled through this study (from coastal and desert locations) in Libya demonstrated that, they show a distinct geographical pattern and differ from all other North Africa *Tarentola* population by at least in some characters, in respect of external morphological characters (see tables 6 and 7, results of T-test and Mann-Whitney test respectively). The correlation of individual values was checked. The correlations between male and female pattern of among site divergence in body dimensions was significant, indicating that the level of similarity was not high; on the basis of the results of ANOVA (table 8 and 9), characters showing significant among group variation, which met the defined criteria, were utilized in further analysis (Linear Discriminant function analysis and Principle component analysis).

Table 4. Morphometric measurements (in mm) of North African *Tarentola* (mean ± SD, for males and females separately).

	T. deserti-NW Africa		*T. deserti*-Libya		*T. sp*-Ras Lanuf		*T. sp*- Sister gr. Ras Lanuf		*T. sp*-complex-Libya		*T. sp*-Sabha		*T. m. fascicularis*-Libya		*T. mauritanica*-Morocco	
	Males N=13 mean±SD	Females N=10 mean±SD	Males N=19 mean±SD	Females N=54 mean±SD	Males N=2 mean±SD	Females N=5 mean±SD	Males N=4 mean±SD	Females N=11 mean±SD	Males N=36 mean±DS	Females N=104 mean±SD	Males N=5 mean±DS	Females N=3 mean±SD	Males N=3 mean±DS	Females N=12 mean±SD	Males N=12 mean±DS	Females N=16 mean±SD
ED	4.5 ± 0.9	4.2 ± 0.8	3.3 ± 0.8	3.6 ± 0.7	4.5 ±0.6	4.2 ±0.9	4.0 ±0.2	3.2 ±0.6	3.5 ±0.8	3.3 ±0.7	4,3 ± 0,3	3,1 ± 0.7	3,5 ± 0.1	3,6 ± 0.6	4.0 ± 0.6	3.4 ± 0.8
AOL	6.5 ± 2.3	5.4 ± 2.2	4.5 ± 1.6	5.1 ±1.3	7.5 ±1.5	6.7 ±2.8	5.2 ±0.4	4.4 ±1.2	5.2 ±2.4	4.5 ±1.4	6,1 ±0,6	3,5 ± 1.7	5,5 ± 1.3	4,6 ± 1.4	6.0 ± 1.1	4.5 ± 1.0
ASL	7.5 ± 2.3	6.7 ± 2.0	5.6 ± 1.4	5.9 ±1.0	8.8 ±1.0	7.4 ±2.6	6.5 ±0.8	5.3 ±1.2	5.8 ±1.5	5.3 ±1.5	7,3 ±0.9	4,8 ± 1.9	5,5 ± 1.1	5,4 ±1.2	7.2 ± 1.1	5.8 ± 1.3
HLL	32.6 ± 10.5	29.8 ± 8.6	24.0 ± 6.3	26.4 ± 5.0	37.1 ± 6.6	32.2 ± 11.9	28.1 ± 0.9	23.1 ± 5.4	24.8 ± 6.6	22.9 ± 6.4	33,3 ± 2.4	20,8 ± 9.1	26,0 ± 3.1	24,7 ± 5.2	30.6 ± 4.9	24.3 ± 5.6
HDW	2.2 ± 0.6	2.1 ± 0.7	1.8 ± 0.7	2.0 ± 0.6	3.0 ±0.7	2.4 ±0.8	2.3 ±0.2	1.8 ±0.5	1.9 ±0.6	1.6 ±0.6	2,5 ±0.2	1,5 ± 0.8	2,3 ± 0.7	1,9 ± 0.5	2.5 ± 0.4	1.9 ± 0.5
HDL	6.6 ± 2.1	5.7 ± 1.7	4.7 ± 1.2	5.2 ±1.0	7.2 ±1.6	6.4 ±2.8	5.2 ±0.3	4.4 ±0.9	5.0 ±1.4	4.6 ±1.3	7,1 ±0.5	4,6 ± 3.2	5,1 ± 1.0	5,0 ± 1.0	6.5 ± 1.4	5.0 ± 1.6
IOB	9.0 ± 3.1	8.3 ± 2.9	5.9 ±1.8	6.5 ±1.6	9.9 ±1.2	8.8 ±3.7	7.4 ±0.6	6.1 ±1.6	6.2 ±1.9	5.8 ±1.7	8,5 ±0.7	5,4 ± 2.5	7,3 ± 1.1	6,2 ± 1.7	8.1 ± 1.4	6.1 ± 1.2
HWm	15.7 ± 5.6	13.7 ± 4.5	12.0 ± 3.3	13.2 ± 2.7	18.7 ± 2.9	16.2 ± 6.1	14.1 ± 0.5	11.6 ± 2.8	12.4 ± 3.6	11.3 ± 3.3	14,9 ± 1.9	8,9 ± 4.1	13,5 ± 2.5	12,2 ± 3.0	15.1 ± 2.3	11.2 ± 1.8
HHm	9.2 ± 3.1	7.8 ± 2.8	6.9 ± 2.0	7.6 ± 1.8	11.0 ±1.5	9.6 ±3.7	8.3 ±0.3	6.7 ±1.9	7.0 ±2.1	7.4 ±9.6	9,2 ± 1.2	5,3 ± 2.5	8,2 ± 1.7	7,0 ± 2.0	8.5 ± 1.0	6.3 ± 1.0
HL	20.8 ± 5.8	18.9 ± 4.8	16.3 ± 3.9	17.6 ± 3.0	23.0 ± 3.2	20.5 ± 6.8	18.5 ± 1.0	16.0 ± 3.4	17.0 ± 3.9	16.5 ± 9.3	19,6 ± 1.7	12,9 ± 4.9	17,8 ± 3.6	16,7 ± 3.4	20.6 ± 2.8	16.1 ± 2.3
SVL	66.4±21.1	60.6 ± 18.0	51.3 ± 13.9	56.0 ±10.7	76.5 ± 13.5	68.9 ± 24.5	71.3 ±20.5	50.6 ±12.1	54.0 ± 14.5	49.6 ±14.3	65,8 ± 6.8	38,7 ±19.1	57,7 ± 10.9	53,0 ± 11.5	65.6 ± 9.7	51.8 ± 9.0
MOL	18.4 ± 5.1	16.9 ± 4.6	10.8 ± 2.9	11.8 ± 2.4	15.9 ± 2.2	13.9 ± 4.8	12.5 ± 0.5	10.4 ± 2.5	11.1 ± 2.7	10.5 ± 2.8	17,7 ± 1.4	12,2 ± 6.5	12,1 ± 1.9	11,0 ± 2.5	17.5 ± 2.7	14.2 ± 2.7
FLL	24.5 ± 7.8	23.0 ± 6.4	18.6 ± 5.1	20.4 ± 4.1	27.9 ± 4.7	24.8 ± 8.7	22.0 ± 1.9	17.9 ± 4.5	19.1 ± 4.8	18.3 ± 9.6	24,5 ± 2.3	15,0 ± 7.2	21,4 ± 2.9	19,9 ± 4.7	22.8 ± 3.8	18.5 ± 4.3
FHLL	31.5 ±10.8	28.6 ± 8.7	22.8 ± 5.9	26.4 ± 5.8	42.6 ± 3.8	28.8 ± 8.9	26.6 ± 8.9	30.6 ± 8.7	24.9 ±6.4	22.8 ± 6.2	31,1 ± 2.6	18,7 ± 7.9	24.9 ± 3.4	25.1 ± 4.3	30.3 ± 4.8	23.3 ± 5.0

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Table 4. Continued

	T. mauritanica- Tunisia		*T. mauritanica*- Algeria		*T. sp*- Tunisia		*T. m. juliae*- Morocco		*T. boehmei*- Morocco		*T. m. fascicularis*- Egypt		*T. mauritanica*- Tripolitania	
	Males N=12 mean±SD	Females N=10 mean±SD	Males N=4 mean±SD	Females N=5 mean±SD	Males N=9 mean±SD	Females N=6 mean±SD	Males N=12 mean±SD	Females N=9 mean±SD	Males N=5 mean±DS	Females N=8 mean±SD	Males N=2 mean±DS	Females N=2 mean±SD	Males N=4 mean±DS	Females N=6 mean±SD
ED	3.7 ± 0.6	3.3 ± 0.6	3.7 ± 0.2	3.3 ± 0.5	3.9 ± 0.4	3.9 ± 0.4	4.0 ± 1.4	3.7 ± 0.7	3.7 ± 0.9	3.7 ± 0.5	3.0 ± 1.0	3.5 ± 0.7	4.3 ± 0.8	3.8 ± 0.4
AOL	5.9 ± 1.6	4.2 ± 0.8	6.0 ± 0.8	4.9 ± 0.8	4.8 ± 1.1	4.6 ± 0.8	4.5 ± 1.2	4.5 ± 1.6	4.2 ±1.0	4.3 ± 0.8	4.6 ± 1.4	4.7 ± 1.2	6.0 ± 1.5	4.9 ± 0.9
ASL	7.3 ± 1.9	5.5 ± 1.2	7.4 ± 0.8	6.0 ± 1.2	5.8 ± 1.0	5.7 ± 0.8	6.3 ± 1.2	6.2 ± 1.2	5.5 ± 0.8	5.7 ± 1.1	4.8 ± 1.3	5.7 ± 0.4	6.7 ± 1.7	5.7 ± 1.0
HLL	29.1 ± 6.1	23.1 ± 4.5	30.7 ± 3.2	25.6 ± 4.9	27.4 ± 3.5	26.9 ± 3.7	27.2 ± 6.1	26.2 ± 5.3	24.4 ± 5.8	25.1 ± 4.4	22.5 ± 8.5	24.6 ± 3.1	29.9 ± 7.1	26.0 ±4.5
HDW	2.5 ± 0.7	1.8 ± 0.5	2.6 ± 0.1	1.9 ± 0.6	1.8 ± 0.5	1.5 ± 0.3	1.9 ± 0.6	1.8 ± 0.4	1.7 ± 0.3	1.9 ± 0.4	1.6 ± 0.7	1.6 ± 0.3	1.4 ± 0.4	1.5 ± 0.5
HDL	6.0 ± 1.6	4.6 ± 0.9	6.5 ± 0.7	5.3 ± 1.2	5.4 ± 1.0	4.6 ± 1.0	5.0 ± 1.1	5.1 ± 1.1	4.6 ± 1.2	4.4 ± 0.9	4.5 ± 1.0	5.0 ± 1.0	5.6 ± 2.1	4.9 ± 1.2
IOB	8.1 ± 1.8	6.3 ± 1.3	8.1 ± 1.3	6.7 ± 1.6	7.4 ± 1.6	7.0 ± 1.2	7.0 ± 2.1	6.6 ± 1.7	6.2 ± 1.4	6.1 ± 1.1	6.0 ± 2.6	7.6 ± 0.7	8.3 ± 2.7	6.9 ± 1.2
HWm	14.8 ± 3.5	11.2 ± 2.4	15.4 ± 1.7	12.5 ± 2.9	12.7 ± 2.5	11.4 ± 1.9	12.5 ± 3.0	11.5 ± 2.7	11.5 ± 2.9	11.5 ± 2.0	10.2 ± 4.0	12.1 ± 1.8	14.2 ± 4.0	11.6 ± 2.0
HHm	8.5 ± 2.1	6.3 ± 1.4	8.4 ± 1.2	6.9 ± 1.4	7.4 ± 1.6	7.1 ± 1.2	6.9 ± 1.9	6.5 ± 1.7	6.2 ± 1.5	6.6 ± 1.2	6.6 ± 2.5	7.0 ± 0.8	7.6 ± 2.0	6.8 ± 1.0
HL	19.7 ± 4.0	15.5 ± 3.3	21.1 ± 1.6	16.9 ± 3.5	17.4 ± 2.2	16.9 ± 2.3	17.5 ± 3.5	16.6 ± 3.0	16.1 ± 2.9	16.5 ± 2.8	14.9 ± 2.9	16.1 ± 2.4	20.0 ± 4.4	17.2 ± 2.6
SVL	62.7 ±14.2	49.7 ± 9.4	67.0 ± 5.8	55.9 ± 12.1	57.8 ± 7.4	53.5 ± 7.8	56.8 ± 12.5	53.5 ±9.9	51.1 ±10.7	53.7 ± 8.3	44.3 ± 15.8	51.1 ± 6.6	63.2 ± 15.2	55.4 ± 9.6
MOL	17.2 ± 3.6	13.6 ± 2.6	17.8 ± 1.8	14.7 ± 2.5	15.8 ± 2.0	15.1 ± 1.8	15.5 ± 3.2	14.5 ±2.5	13.8 ± 2.4	14.6 ± 2.3	12.7 ± 4.1	14.7 ± 2.8	17.3 ± 4.8	15.1 ± 2.2
FLL	21.4 ±4.4	17.3 ± 3.1	23.3 ± 1.2	18.8 ± 4.3	21.0 ± 3.0	19.4 ± 2.2	20.1 ± 4.1	19.5 ±3.9	17.9 ± 3.9	19.0 ± 3.2	16.9 ± 4.5	18.3 ±3.8	23.0 ± 6.0	20.7 ± 2.8
FHLL	29.6 ± 7.5	23.1 ± 4.9	32.0 ± 2.4	26.2 ± 6.90	25.0 ± 3.3	23.9 ± 4.2	25.8 ± 5.0	24.5 ±5.3	23.1 ± 5.0	24.6 ± 4.6	20.1 ± 8.3	23.6 ±2.7	28.5 ± 5.7	23.6 ± 3.6

Note: *T.neglecta*-South Libya and *T.sp*-Sister group. Sabha not included here, because of low specimens number.

Table 5. Meristic characters of North African *Tarentola* (mean ± SD).

characters	*T. sp*-complex-Libya N=139 mean±SD	*T. deserti*-Libya N=73 mean±SD	*T. deserti*-N Africa N=24 mean±SD	*T. sp*- sister gr. Sabha N=4 mean±SD	*T. sp*- Ras Lanuf-Libya N=6 mean±SD	*T. sp*- sister gr. Ras Lanuf N=15 mean±SD	*T. m. fascicularis*-Libya N=15 mean±SD	*T. neglecta*- S-Libya N=3 mean±SD
1st toe	10.9 ± 0.6	11.0 ± 0.7	12.7 ± 1.1	11.2 ± 0.5	11.7 ± 0.5	10.7 ± 0.9	9.3 ± 0.8	10.0 ± 0.0
4th toe	15.8 ± 1.0	15.9 ± 0.8	18.2 ± 1.3	17.5 ± 1.0	17.7 ± 0.5	15.7 ± 1.5	14.4 ± 1.2	15.0 ± 0.0
5th toe base	20.2 ± 1.6	20.3 ± 1.1	22.8 ± 1.3	22.0 ± 0.8	22.5 ± 0.5	20.8 ± 1.6	19.7 ±1.5	18.0 ± 0.0
VS	36.6 ± 3.2	40.0 ± 2.7	40.1 ± 2.0	38.0 ± 2.7	39.8 ± 1.9	36.5 ± 1.9	36.7 ± 3.5	42.7 ± 0.6
Cr	5.7 ± 0.6	5.7 ± 0.5	6.2 ± 0.5	5.5 ± 1.0	6.0 ± 0.6	5.5 ± 0.5	6.1 ± 2.5	5.0 ± 0,0
DT	12.8 ±1.4	13.4 ± 0.9	12.2 ± 0.7	13.5 ± 1.0	14.0 ± 0.0	13.4 ±1.0	13.1 ± 3.3	13.0 ± 0.0
GS	43.3 ± 4.7	45.3 ± 5.4	56.0 ± 6.9	50.0 ±2.4	48.2 ± 6.5	43.9 ± 3.6	42.2 ± 4.0	47.3 ± 4.9
IOA	14.9 ± 0.7	14.6 ± 0.9	14.5 ±0.7	14.0 ± 1.4	13.8 ± 1.5	13.7 ±1.0	14.2 ± 1.1	13.3 ± 0.6
Sub	7.9 ± 0.5	8.0 ± 0.5	8.8 ± 0.6	7.7 ± 0.5	8.0 ± 0.9	7.7 ±0.5	7.7 ± 0.6	8.0 ± 0.0
Supra	7.9 ± 0.5	8.0 ± 0.4	8.0 ± 0.4	7.5 ± 0.6	7.5 ± 0.5	7.1 ±0.2	7.2 ± 0.6	9.0 ± 0.0
characters	*T. sp*-Sabha-S Libya N=8 mean±SD	*T. mauritanica* Morocco N=28 mean±SD	*T. mauritanica* - Tunisia N=22 mean±SD	*T. mauritanica*- Algeria N=9 mean±SD	*T. sp*- Tunisia N=15 mean±SD	*T. m. juliae*- Morocco N=18 mean±SD	*T. boehmei*- Morocco N=13 mean±SD	*T. m. fascicularis*- Egypt N=4 mean±SD
1st toe	13.0 ± 0.7	11.1 ± 1.4	11.0 ± 1.0	10.9 ± 0.9	10.3 ± 0.8	11.2 ± 0.8	11.6 ± 0.6	10.0 ± 0.0
4th toe	18.2 ± 0.9	16.3 ± 1.2	16.8 ± 1.0	17.0 ± 1.8	15.3 ± 1.0	17.6 ± 1.6	17.3 ± 0.9	14.2 ± 0.9
5th toe base	22.1 ± 1.1	20.2 ±1.3	20.5 ± 1.5	20.8 ± 1.7	19.7 ± 1.1	21.4 ± 1.7	21.6 ± 1.1	18.2 ± 0.5
VS	41.7 ±1.6	36.8 ± 3.9	37.7 ± 3.3	35.3± 1.6	34.3 ± 2.7	37.7 ± 4.5	43.8 ± 2.2	34.2 ± 0.9
Cr	6.4 ±0.5	5.7 ± 0.6	5.8 ± 0.5	5.5 ± 0.7	5.7 ± 0.4	5.6 ± 0.5	6.1 ± 0.5	5.2 ± 0.5
DT	14.0 ±0.7	13.3 ± 1.2	13.5 ± 1.0	14.4 ± 0.9	12.1 ± 0.5	12.0 ± 0.2	12.0 ± 0.0	12.0 ± 0.0
GS	47.6 ±1.6	40.6 ± 4.7	41.1 ± 4.7	42.4 ± 6.9	43.3 ± 6.6	42.9 ± 6.0	50.5 ± 5.6	40.7 ± 3.4
IOA	14.6 ± 0.7	14.8 ± 1.1	14.9 ± 1.2	14.8 ± 0.8	13.7 ± 1.0	14.8 ± 1.2	15.6 ± 0.9	13.7 ± .05
Sub	7.9 ± 0.8	8.2 ± 0.6	8.0 ± 0.7	7.9 ± 0.6	7.9 ± 0.7	7.9 ± 0.4	8.8 ± 0.4	7.5 ± 0.6
Supra	9.2 ± 0.5	8.9 ± 1.5	7.8 ± 0.6	7.8 ± 0.7	7.7 ± 0.7	7.9 ± 0.5	8.3 ± 0.5	6.5 ± 0.6

characters	*T. mauritanica*- Tripolitania N=8 mean±SD
1st toe	11.2 ± 0.7
4th toe	16.2 ± 1.1
5th toe base	21.0 ± 1.6
VS	37.1 ± 2.3
Cr	6.1 ± 0.3
DT	11.2 ± 1.0
GS	44.4 ± 4.6
IOA	14.4 ± 0.9
Sub	8.7 ± 0.7
Supra	8.1 ± 0.6

Table 6. Selection of T-test results of the morphometric and meristic characters, for males and females separately (the left values refers to comparison among males, and the right values to comparison among females), between several groups of North African *Tarentola*: n.s, P>0.05= not significant; *, P<0.05; **, P<0.01; ***, P<0.001.

	T. deserti-Libya X *T .deserti*-NW Africa	*T. deserti*-Libya X *T. sp*-Tunisia	*T. deserti*-Libya X *T. mauritanica*-*Tunisia*	*T. deserti*-Libya X *T. mauritanica*-*Algeria*	*T. deserti*-Libya X *T. sp*-complex-Libya	*T. deserti*-Libya X *T. sp*-Ras Lanuf	*T. deserti*-Libya X *T. sp*-sister gr. Ras Lanuf	*T. deserti*-Libya X *T. m. fascicularis*-Libya	*T. deserti*-Libya X *T. sp*-Suirt-sister gr. Sabha	*T. deserti*-Libya X *T.sp*-Sabha-South Libya	*T. sp-complex-Libya X T. deserti*-NW Africa	*T. sp*-complex-Libya X *T. sp*-Tunisia
1st toe	*** / ***	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / *	*** / ***	n.s / n.s	*** / n.s	*** / ***	n.s / ***
4th toe	*** / ***	n.s / **	*** / n.s	n.s / **	n.s / n.s	*** / n.s	* / **	** / ***	** / **	*** / n.s	*** / ***	n.s / *
5th toe base	*** / ***	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / **	** / n.s	*** / ***	n.s / n.s
VS	n.s / n.s	*** / ***	n.s / ***	*** / ***	*** / ***	n.s / n.s	** / ***	n.s / ***	n.s / n.s	n.s / n.s	*** / ***	*** / n.s
Cr	* / **	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / *	* / n.s	n.s / ***	n.s / n.s
DT	*** / ***	** / ***	n.s /n.s	** / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
GS	*** / ***	* / n.s	n.s / **	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / ***	n.s / n.s
IOA	n.s / n.s	** / **	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	*** / ***
MS	n.s / **	n.s / n.s	n.s / *	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s
Sublabialia	*** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / *	n.s / n.s	n.s / *	*** / ***	n.s / n.s
Supralabialia	n.s / n.s	n.s / *	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	*** / ***	** / ***	n.s / *	*** / *	n.s / n.s	n.s / n.s
RelED	* / **	* / **	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelAOL	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s
RelASL	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	* / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s
RelHLL	** /**	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	** / *	*** / **	n.s / **
RelHDW	n.s / n.s	n.s / ***	** / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **
RelHDL	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	** / n.s	* / n.s	n.s / *
RelIOB	*** / ***	*** / *	*** / *	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	* / n.s	n.s / n.s	*** / n.s	*** / n.s	*** / n.s
RelHWm	n.s / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / ***	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s
RelHHm	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	* / n.s	n.s / n.s
RelHL	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / ***	n.s / n.s	* / n.s
RelSVL	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / **	n.s / n.s	* / n.s
RelMOL	*** / ***	*** / ***	*** / ***	*** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / n.s	*** / **	*** / **
RelFLL	n.s / **	n.s / n.s	* / *	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s
RelFHLL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s

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Table 6. Continued

	T.sp-complex-Libya X *T.mauritanica*-*Tunisia*	*T.sp*-complex-Libya X *T.mauritanica*-*Algeria*	*T.sp*-complex-Libya X *T. sp*-Ras Lanuf	*T.sp*-complex-Libya X *T.sp*-sister gr.Ras Lanuf	*T. sp*-complex-Libya X *T.m.fascicularis* -Libya	*T.sp*-complex-Libya X *T.sp*-Sabha-South Libya	*T. sp*-Ras Lanuf-Libya X *T. deserti*-NW Africa	*T. sp*-Ras Lanuf-Libya X *T. sp*-Tunisia	*T. sp*-Ras Lanuf-Libya X *T.mauritanica*-Tunisia	*T. sp*-Ras Lanuf-Libya X *T.mauritanica*-Algeria	*T. sp*-Ras Lanuf X *T. sp*-sister group Ras Lanuf-Libya	*T. sp*-Ras Lanuf X *T.m.fascicularis*-Libya
1st toe	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	*** / ***	*** / ***	n.s / ***	* / **	n.s / n.s	n.s / n.s	n.s / *	- / ***
4th toe	*** / n.s	n.s / **	*** / n.s	** / n.s	** / ***	*** / ***	n.s / n.s	** / *	n.s / n.s	n.s / n.s	n.s / *	** / **
5th toe base	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s
VS	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / **	n.s / n.s	** / **	n.s / n.s	* / **	n.s / **	n.s / *
Cr	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
DT	* / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / *	** / ***	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s
GS	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
IOA	n.s / n.s	n.s / n.s	n.s / *	** / ***	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
MS	n.s /*	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
Sublabialia	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
Supralabialia	n.s / n.s	n.s / n.s	n.s / n.s	*** / ***	* / ***	*** / ***	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s
RelED	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelAOL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / **	n.s / n.s	** / **	n.s / **
RelASL	*** / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	* / n.s	n.s / n.s	* / n.s	n.s / **	** / **
RelHLL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / ***	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHDW	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHDL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	*** / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelIOB	*** / n.s	n.s / n.s	* / n.s	n.s / n.s	* / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *
RelHWm	n.s / n.s	n.s / n.s	* / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* /**	n.s / **	** / n.s	* / n.s	n.s / n.s
RelHHm	n.s / n.s	n.s / n.s	** / *	* / n.s	* / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / *	* / n.s	* / n.s	n.s / n.s
RelHL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelSVL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelMOL	*** / **	*** / *	n.s / n.s	n.s / n.s	n.s / n.s	*** / n.s	*** / ***	*** /***	*** / ***	** / ***	n.s / n.s	n.s / n.s
RelFLL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelFHLL	n.s / n.s	n.s / n.s	** / n.s	n.s / ***	n.s / n.s	n.s / n.s	** / n.s	** / n.s	** / n.s	n.s / n.s	n.s / *	* / n.s

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Table 6. Continued

	T. sp-Ras Lanuf X *T. sp*-Sabha-South Libya	*T. sp*-sister gr. Ras Lanuf-Libya X *T. deserti*-NW Africa	*T. sp*-sister gr. Ras Lanuf-Libya X *T. sp*-Tunisia	*T. sp*-sister gr. Ras Lanuf-Libya X *T. mauritanica*-Tunisia	*T. sp*-sister gr. Ras Lanuf-Libya X *T. mauritanica*-Algeria	*T. sp*-sister gr. Ras Lanuf-Libya X *T.m.fascicularis*-Libya	*T. sp*-sister gr. Ras Lanuf-Libya X *T. sp*-Sabha-South Libya	*T.m.fascicularis*-Libya X *T. deserti*-NW Africa	*T.m.fascicularis*-Libya X *T. sp*-Tunisia	*T.m.fascicularis*-Libya X *T. mauritanica*-Tunisia	*T.m.fascicularis*-Libya X *T. mauritanica*-Algeria	*T.m.fascicularis*-Libya X *T. sp*-Sabha-South Libya
1st toe	n.s / *	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	*** / **	** / n.s	*** / ***	* / n.s	** / **	* / **	*** / ***
4th toe	n.s / n.s	n.s / ***	n.s / n.s	n.s / **	n.s / **	n.s / n.s	n.s / n.s	*** / ***	n.s / n.s	*** / ***	n.s / **	*** / ***
5th toe base	n.s / n.s	n.s / ***	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / ***	n.s / n.s	n.s / n.s	n.s / *	** / *
VS	n.s / n.s	** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / **	** / n.s	n.s / n.s	** / n.s	n.s /**
Cr	n.s / n.s	** / ***	** / n.s	* / n.s	* / n.s	n.s / n.s	** / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s
DT	n.s / n.s	* / **	n.s /**	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	*** / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / n.s
GS	n.s / n.s	* / ***	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	** / ***	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s
IOA	n.s / n.s	* / n.s	n.s / n.s	n.s / **	n.s / **	n.s / n.s	n.s / n.s	n.s /n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
MS	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / *	n.s / *	n.s / n.s
Sublabialia	n.s / n.s	** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
Supralabialia	** / **	*** / ***	** / n.s	** / **	n.s / **	n.s / n.s	*** / ***	* / ***	n.s / n.s	n.s / *	n.s / *	** / ***
RelED	* / n.s	n.s / *	n.s / **	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelAOL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelASL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	* / *	n.s / n.s	** / **	** / **	*** / ***
RelHLL	n.s / n.s	n.s / ***	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	* / **	n.s / ***	n.s / n.s	n.s / n.s	* / ***
RelHDW	n.s / *	n.s / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s
RelHDL	* / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	*** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s
RelIOB	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s /**	n.s / *	n.s / n.s	n.s / n.s
RelHWm	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHHm	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelSVL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelMOL	*** / **	*** / ***	** / ***	*** / ***	*** / ***	n.s / n.s	*** / ***	*** / ***	*** / ***	*** / ***	** / ***	*** / ***
RelFLL	n.s / n.s	n.s / ***	n.s / n.s	** / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	* / **	n.s / ***	n.s / n.s
RelFHLL	** / n.s	n.s / *	n.s / *	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s

…..continued on the next page

Table 6. Continued

	T.m.fascicularis-Libya X *T.m.fascicularis*-Egypt	*T. sp*-Sabha South Libya X *T. deserti*-NW Africa	*T. sp*-Sabha South Libya X *T. sp*-Tunisia	*T. sp*-Sabha South Libya X *T.mauritanica*-Tunisia	*T. sp*-Sabha South Libya X *T. mauritanica*-Algeria	*T. mauritanica*-Morocco *X T. mauritanica*-Algeria	*T. mauritanica*-Morocco *X T. mauritanica*-Tunisia	*T. mauritanica*-Morocco *X T.sp*-complex-Libya	*T. mauritanica*-Morocco *X T. m. juliae*-Morocco	*T. mauritanica*-Morocco *X T. boehmei*-Morocco	*T. m. juliae*-Morocco *X T. boehmei*-Morocco
1st toe	n.s / n.s	n.s / n.s	*** / ***	** / **	** / *	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s
4th toe	n.s / n.s	n.s / n.s	*** / **	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / **	n.s / n.s
5th toe base	n.s / n.s	n.s / n.s	*** / *	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s
VS	** / n.s	n.s / n.s	*** / *	* / n.s	*** / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / ***	*** / n.s
Cr	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s
DT	n.s / n.s	*** / *	*** / ***	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	** / ***	* / **	n.s / n.s
GS	n.s / n.s	n.s / **	n.s / n.s	* / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	* / ***	n.s / **
IOA	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s
MS	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s
Sublabialia	n.s / n.s	* / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	** / n.s	** / **
Supralabialia	n.s / **	*** / ***	*** / **	*** / ***	*** / n.s	n.s / n.s	n.s / **	** / ***	n.s / *	n.s / n.s	n.s / n.s
RelED	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	** / n.s	n.s / n.s
RelAOL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	* / n.s	n.s / n.s
RelASL	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHLL	n.s / n.s	n.s / **	** / n.s	** / ***	** / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHDW	n.s / n.s	* / ***	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	*** / n.s	** / n.s	n.s / n.s
RelHDL	n.s / n.s	n.s / *	** / *	** / *	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / *	n.s / **
RelIOB	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHWm	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHHm	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHL	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelSVL	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelMOL	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	* / n.s	*** / ***	** / n.s	n.s / n.s	n.s / n.s
RelFLL	n.s / n.s	n.s / n.s	n.s / n.s	** / *	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelFHLL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s /	n.s / n.s	n.s / n.s

Table 7. Selection of Mann-Whitney U Test results of morphometric and meristic characters, for males and females separately (the left values refers to comparison among males, and the right values to comparison among females), between several groups of North African *Tarentola*: n.s, P>0.05= not significant; *, P<0.05; **, P<0.01; ***, P<0.001.

	T. deserti-Libya X *T. deserti*-NW Africa	*T. deserti*-Libya X *T. sp*-Tunisia	*T. deserti*-Libya X *T. mauritanica*-*Tunisia*	*T. deserti*-Libya X *T.mauritanica*-*Algeria*	*T. deserti*-Libya *X T. sp*-complex-Libya	*T. deserti*-Libya X *T. sp*-Ras Lanuf	*T. deserti*-Libya X *T. sp*- sister gr. Ras Lanuf	*T. deserti*-Libya X *T.m.fascicularis*-Libya	*T. deserti*-Libya X *T. sp*-Suirt-sister gr.Sabha	*T. deserti*-Libya X *T.sp*-Sabha-South Libya	*T.sp-complex-Libya X T. deserti*-NW Africa	*T.sp*-complex-Libya X *T.sp*-Tunisia
1st toe	*** / ***	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / ***	- / n.s	*** / ***	*** / ***	n.s / **
4th toe	*** / ***	n.s / **	** / n.s	n.s / n.s	n.s / *	** / n.s	n.s / **	** / ***	- / n.s	*** / **	*** / ***	n.s / n.s
5th toe base	*** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / *	n.s / n.s	n.s / n.s	- / **	** / n.s	*** / ***	n.s / n.s
VS	n.s / n.s	*** / ***	n.s / **	*** / ***	*** / ***	n.s / n.s	* / ***	n.s / ***	- / n.s	n.s / n.s	*** / **	** / n.s
Cr	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / *	n.s / n.s	n.s / **	n.s / n.s
DT	** / **	* / ***	n.s / n.s	* / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	n.s / n.s	* / n.s	n.s / n.s
GS	*** / ***	n.s / n.s	n.s / **	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / **	- / n.s	n.s / n.s	*** / ***	n.s / n.s
IOA	n.s /n.s	* / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	- / n.s	n.s / n.s	n.s / *	** / ***
MS	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	n.s / n.s	n.s / **	n.s / n.s
Sublabialia	*** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	- / n.s	n.s / n.s	*** / ***	n.s / n.s
Supralabialia	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / ***	n.s / ***	- / n.s	*** / ***	n.s / n.s	n.s / n.s
RelED	n.s / **	* / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	n.s / *	n.s / *	n.s / **
RelAOL	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	** / n.s	n.s / n.s	n.s / n.s
RelASL	* / n.s	n.s / n.s	** / n.s	n.s / *	n.s / n.s	* / *	n.s / n.s	** / n.s	- / n.s	** / n.s	n.s / n.s	n.s / n.s
RelHLL	** / **	n.s / ***	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / **	n.s / n.s	- / n.s	** / ***	*** / **	n.s / ***
RelHDW	n.s / n.s	n.s / ***	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	n.s / n.s	n.s / n.s	* / **
RelHDL	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / **	*** / *	* / n.s	n.s / *
RelIOB	*** / **	*** / **	*** / *	n.s / n.s	n.s / ***	** / *	* / n.s	* / n.s	- / n.s	*** / n.s	*** / **	*** / **
RelHWm	n.s / n.s	n.s / ***	n.s / *	n.s / n.s	n.s / *	** / n.s	n.s / n.s	n.s / n.s	- / n.s	n.s / *	n.s / n.s	n.s / n.s
RelHHm	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	* / n.s	n.s / n.s	n.s / n.s	- / n.s	** / n.s	** / n.s	n.s / n.s
RelHL	n.s / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	*** / n.s	n.s / n.s	** / n.s
RelSVL	n.s / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	*** / n.s	n.s / n.s	** / n.s
RelMOL	*** / ***	*** / ***	*** / ***	*** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	*** / **	*** / ***	*** / ***
RelFLL	n.s / **	n.s / n.s	* / *	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	- / n.s	n.s / n.s	n.s / **	n.s / n.s
RelFHLL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	- / *	n.s / n.s	n.s /	* / n.s

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Table 7. Continued

	T sp-complex-Libya X *T.mauritanica-Tunisia*	*T.sp*-complex-Libya X *T.mauritanica-Algeria*	*T.sp*-complex-Libya X *T. sp*-Ras Lanuf	*T.sp*-complex-Libya X sister gr. *T.sp*-Ras Lanuf	*T.sp*-complex-Libya X *T.m.fascicularis*-Libya	*T. sp*-complex-Libya X *T.sp*-Sabha-South Libya	*T. sp*-Ras Lanuf-Libya X *T. deserti*-NW Africa	*T. sp*-Ras Lanuf-Libya X *T. sp*-Tunisia	*T. sp*-Ras Lanuf-Libya X *T.mauritanica*-Tunisia	*T. sp*-Ras Lanuf-Libya X *T.mauritanica*-Algeria	*T. sp*-Ras Lanuf X *T.sp*-sister gr. Ras Lanuf-Libya	*T. sp*-Ras Lanuf X *T.m.fascicularis*-Libya
1st toe	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	** / ***	*** / ***	n.s / **	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **
4th toe	*** / *	n.s / n.s	** / n.s	n.s / n.s	** / ***	*** / **	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *
5th toe base	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
VS	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	*** / **	n.s / n.s	* / **	n.s / n.s	n.s / **	n.s / *	n.s / n.s
Cr	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
DT	n.s / n.s	** / *	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	* / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
GS	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
IOA	n.s / n.s	n.s / n.s	n.s / n.s	n.s / ***	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
MS	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
Sublabialia	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
Supralabialia	n.s / n.s	n.s / n.s	n.s / n.s	** / ***	n.s / ***	*** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelED	n.s / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelAOL	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / *	n.s / **
RelASL	** / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / **
RelHLL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	*** / ***	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHDW	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHDL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	*** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelIOB	*** / ***	n.s / n.s	** / *	n.s / n.s	* / n.s	*** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHWm	n.s / n.s	n.s / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHHm	n.s / n.s	n.s / n.s	** / *	** / n.s	n.s / n.s	*** / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / *
RelHL	n.s / n.s	n.s / *	n.s / *	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelSVL	n.s / n.s	n.s / *	n.s / *	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelMOL	*** / ***	*** / ***	n.s / *	n.s / n.s	n.s / n.s	*** / **	** / ***	* / **	* / ***	n.s / **	n.s / n.s	n.s / n.s
RelFLL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelFHLL	n.s / n.s	n.s / n.s	** / n.s	n.s / ***	n.s / n.s	n.s / n.s	* / n.s	* / n.s	* / n.s	n.s / n.s	n.s / **	n.s / n.s

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Table 7. Continued

	T. sp-Ras Lanuf X *T. sp*-Sabha-South Libya	*T. sp*-sister gr. Ras Lanuf-Libya X *T. deserti*-NW Africa	*T. sp*-sister gr. Ras Lanuf-Libya X *T. sp*-Tunisia	*T. sp*-sister gr.Ras Lanuf-Libya X *T. mauritanica*-Tunisia	*T. sp*-sister gr. Ras Lanuf-Libya X *T. mauritanica*-Algeria	*T. sp*-sister gr. Ras Lanuf-Libya X *T.m.fascicularis*-Libya	*T. sp*-sister gr. Ras Lanuf-Libya X *T. sp*-Sabha-South Libya	*T.m.fascicularis*-Libya X *T. deserti*-NW Africa	*T.m.fascicularis*-Libya X *T. sp*-Tunisia	*T.m.fascicularis*-Libya X *T. mauritanica*-Tunisia	*T.m.fascicularis*-Libya X *T. mauritanica*-Algeria	*T.m.fascicularis*-Libya X *T. sp*-Sabha-South Libya
1st toe	n.s / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	* / **	** / ***	** / *	** / **	n.s / **	* / **
4th toe	n.s / n.s	n.s / ***	n.s / n.s	n.s / **	n.s / *	n.s / n.s	n.s / **	** / ***	n.s / n.s	** / ***	n.s / **	* / **
5th toe base	n.s / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / ***	n.s / n.s	n.s / n.s	n.s / **	* / n.s
VS	n.s / n.s	* / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / **	n.s / **	** / n.s	n.s / n.s	n.s / n.s	n.s / **
Cr	n.s / n.s	* / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
DT	n.s / n.s	n.s / *	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / **	** / **	n.s / n.s	n.s / n.s	n.s / n.s
GS	n.s / n.s	* / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / ***	n.s / **	n.s / n.s	n.s / n.s	n.s / *
IOA	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / **	n.s / n.s	n.s / n.s	n.s /n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
MS	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s
Sublabialia	n.s / n.s	** / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
Supralabialia	n.s / *	** / ***	* / n.s	* / **	n.s / **	n.s / n.s	** / **	n.s / ***	n.s / n.s	n.s / n.s	n.s / *	* / **
RelED	n.s / n.s	n.s / *	n.s / **	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelAOL	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelASL	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / **	n.s / n.s	n.s / *	* / n.s	n.s / n.s	** / *	n.s /**	* / *
RelHLL	n.s / *	n.s / ***	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / **	n.s / ***	n.s / n.s	n.s / n.s	n.s / **
RelHDW	n.s / *	* / n.s	* / ***	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / ***	n.s / n.s	n.s / n.s	n.s / n.s
RelHDL	n.s / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	** / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelIOB	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / **	n.s / *	n.s / n.s	n.s / n.s
RelHWm	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHHm	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelSVL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / v	n.s / n.s	n.s / n.s	n.s / n.s
RelMOL	n.s / *	*** / ***	** / ***	** / ***	* / ***	n.s / n.s	** / **	** / ***	** / ***	** / ***	n.s / ***	* / **
RelFLL	n.s / n.s	n.s / ***	n.s / n.s	* / n.s	n.s / n.s	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / **	n.s / n.s
RelFHLL	n.s / n.s	n.s / **	n.s / *	n.s / **	n.s / *	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s

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Table 7. Continued

	T.m.fascicularis -Libya X *T.m.fascicularis* -Egypt	*T. sp*-Sabha South Libya X *T. deserti*-NW Africa	*T. sp*-Sabha South Libya X *T. sp*-Tunisia	*T. sp*-Sabha South Libya X *T. mauritanica*-Tunisia	*T. sp*-Sabha South Libya X *T. mauritanica*-Algeria	*T. mauritanica*-Morocco *X T. mauritanica*-Algeria	*T. mauritanica*-Morocco *X T. mauritanica*-Tunisia	*T. mauritanica*-Morocco *X T. sp*-complex-Libya	*T. mauritanica*-Morocco *X T. m. juliae*-Morocco	*T. mauritanica*-Morocco *X T. boehmei*-Morocco	*T. m. juliae*-Morocco *X T. boehmei*-Morocco
1st toe	n.s / n.s	n.s / n.s	*** / *	** / **	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
4th toe	n.s / n.s	n.s / n.s	*** / *	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / **	n.s / n.s
5th toe base	n.s / n.s	n.s / n.s	*** / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / **	n.s / n.s
VS	n.s / n.s	n.s / n.s	*** / *	** / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / ***	*** / n.s
Cr	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
DT	n.s / n.s	*** / n.s	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / **	* / **	n.s / -
GS	n.s / n.s	* / *	* / n.s	* / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / ***	n.s / **
IOA	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
MS	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s
Sublabialia	n.s / n.s	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	** / *
Supralabialia	n.s / *	*** / **	*** / *	** / **	** / n.s	n.s / n.s	n.s / **	n.s / **	n.s / n.s	n.s / n.s	n.s / n.s
RelED	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	** / n.s	n.s / n.s
RelAOL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s
RelASL	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHLL	n.s / n.s	n.s / *	* / *	** / **	* / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHDW	n.s / n.s	** / **	** / *	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	*** / n.s	*** / n.s	n.s / n.s	n.s / n.s
RelHDL	n.s / n.s	n.s / n.s	** / n.s	** / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / *	n.s / **
RelIOB	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHWm	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHHm	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelHL	n.s / n.s	** / n.s	n.s / n.s	** / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelSVL	n.s / n.s	** / n.s	n.s / n.s	** / n.s	** / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelMOL	n.s / *	n.s / n.s	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	* / n.s	*** / ***	** / n.s	n.s / n.s	n.s / n.s
RelFLL	n.s / n.s	n.s / n.s	n.s / n.s	** / *	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s
RelFHLL	n.s / n.s	n.s / n.s	* / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s	n.s / n.s

Table 8. Summary of One-Way ANOVA analysis of the morphometric and meristic characters among several groups of North African *Tarentola* (males): 1-*T.sp*-complex-Libya, 3-*T.sp*-Suirt Libya, 4-*T.deserti*-Libya, 5-*T.sp*-Ras Lanuf, 6-*T.sp*-sister group Ras Lanuf, 7-*T.m.fascicularis*-Libya, 8-*T.neglecta*-South Libya, 10-*T.sp*-Sabha Libya, 13-*T.mauritanica*-Morocco, 14-*T.mauritanica*-Tripolitania, 18-*T.mauritanica*-Tunisia, 19-*T.sp*-Tunisia, 20- *T.mauritanica*-Algeria, 21-*T.deserti*-North West Africa, 22-*T.m.fascicularis*-Egypt. (Symbols refer to the significant level: n.s, P>0.05= not significant; *, P<0.05; **, P<0.01; ***, P<0.001).

characters	Groups: 1-4-19-21			Groups: 4-7-13-18-20-21			Groups: 4-5-6-13-18-20			Groups: 3-4-10-13-18-20			Groups: 3-4-7-10-13-14-18-20-22			Groups: 1-3-4-5-6-7-8-10		
	df	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*
1.toe	3	19.6	***	5	9.8	***	5	0.8	n.s	5	5.8	***	8	6.6	***	7	10.3	***
4.toe	3	34.9	***	5	10.8	***	5	2.7	*	5	6.1	***	8	6.5	***	7	9.0	***
5.toe	3	17.3	***	5	8.1	***	5	1.7	n.s	5	2.4	n.s	8	3.1	**	7	2.5	**
BS	3	19.3	***	5	6.8	***	5	2.9	**	5	5.3	***	8	4.1	***	7	4.7	***
Cr	3	2.0	n.s	5	1.8	n.s	5	2.1	n.s	5	1.6	n.s	8	2.2	*	7	2.6	**
DT	3	4.0	**	5	10.7	***	5	2.0	n.s	5	3.1	*	8	4.6	***	7	1.0	n.s
GS	3	24.3	***	5	8.2	***	5	1.7	n.s	5	2.2	n.s	8	1.5	n.s	7	2.1	n.s
IOA	3	7.4	***	5	0.1	n.s	5	0.6	n.s	5	0.1	n.s	8	0.5	n.s	7	2.2	*
MS	3	0.6	n.s	5	0.3	n.s	5	0.8	n.s	5	0.9	n.s	8	0.6	n.s	7	1.8	n.s
Sublabialia	3	14.4	***	5	7.5	***	5	0.4	n.s	5	0.5	n.s	8	0.9	n.s	7	0.5	n.s
Supralabialia	3	1.0	n.s	5	3.1	*	5	2.5	*	5	4.2	**	8	3.6	**	7	10.3	***
RelAD	3	2.9	*	5	3.8	**	5	1.2	n.s	5	2.3	n.s	8	1.8	n.s	7	1.2	n.s
RelAOL	3	1.2	n.s	5	2.2	n.s	5	1.7	n.s	5	2.0	n.s	8	1.4	n.s	7	0.5	n.s
RelASL	3	2.3	n.s	5	2.6	*	5	2.4	*	5	3.9	**	8	4.3	***	7	2.5	**
RelHBL	3	7.5	***	5	2.6	n.s	5	0.4	n.s	5	3.7	**	8	2.9	**	7	3.7	***
RelHZB	3	0.7	n.s	5	2.6	n.s	5	2.3	*	5	3.4	**	8	6.3	***	7	1.4	n.s
RelHZL	3	2.7	n.s	5	1.4	n.s	5	0.8	n.s	5	2.8	*	8	2.1	n.s	7	3.6	***
RelIOB	3	12.3	***	5	5.8	***	5	3.7	**	5	7.3	***	8	4.4	***	7	4.2	***
RelKB	3	0.4	n.s	5	0.3	n.s	5	1.7	n.s	5	0.7	n.s	8	1.1	n.s	7	2.4	*
RelKH	3	1.3	n.s	5	2.6	n.s	5	2.1	n.s	5	3.0	*	8	2.2	*	7	2.8	**
RelKL	3	2.8	*	5	0.4	n.s	5	1.0	n.s	5	2.4	n.s	8	2.1	n.s	7	1.6	n.s
RelKRL	3	3.1	*	5	0.5	n.s	5	1.0	n.s	5	2.6	*	8	2.1	n.s	7	1.6	n.s
RelMOL	3	97.0	***	5	61.2	***	5	50.0	***	5	70.3	***	8	42.7	***	7	9.3	***
RelVBL	3	0.9	n.s	5	1.3	n.s	5	1.6	n.s	5	2.7	*	8	2.2	*	7	1.0	n.s
RelVHBL	3	0.4	n.s	5	0.1	n.s	5	0.3	n.s	5	0.02	n.s	8	0.09	n.s	7	0.3	n.s

Table 9. Summary of One-Way ANOVA analysis of the morphometric and meristic characters among several groups of North African *Tarentola* (females): 1-*T.sp*-complex-Libya, 3-*T.sp*-Suirt Libya, 4-*T.deserti*-Libya, 5-*T.sp*-Ras Lanuf, 6-*T.sp*-sister group Ras Lanuf, 7-*T.m.fascicularis*-Libya, 8-*T.neglecta*-South Libya, 10-*T.sp*-Sabha Libya, 13-*T.mauritanica*-Morocco, 14-*T.mauritanica*-Tripolitania, 18-*T.mauritanica*-Tunisia, 19-*T.sp*-Tunisia, 20- *T.mauritanica*-Algeria, 21-*T.deserti*-North West Africa, 22-*T.m.fascicularis*-Egypt. (Symbols refer to the significant level: n.s, P>0.05= not significant; *, P<0.05; **, P<0.01; ***, P<0.001).

characters	Groups: 1-4-19-21			Groups: 4-7-13-18-20-21			Groups: 4-5-6-13-18-20			Groups: 3-4-10-13-18-20			Groups: 3-4-7-10-13-14-18-20-22			Groups: 1-3-4-5-6-7-8-10		
	df	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*	*df*	*F*-ratio	*P*
1.toe	3	41.2	***	5	17.9	***	5	1.6	n.s	5	3.7	**	8	7.5	***	7	13.3	***
4.toe	3	19.3	***	5	16.5	***	5	4.4	***	5	6.2	***	8	8.6	***	7	6.4	***
5.toe	3	9.8	***	5	8.3	***	5	1.4	n.s	5	1.7	n.s	8	2.0	*	7	2.4	**
BS	3	18.3	***	5	8.2	***	5	7.2	***	5	5.7	***	8	5.4	***	7	6.8	***
Cr	3	4.3	**	5	1.3	n.s	5	1.0	n.s	5	2.3	n.s	8	0.8	n.s	7	1.3	n.s
DT	3	7.6	***	5	1.4	n.s	5	0.6	n.s	5	0.9	n.s	8	1.8	n.s	7	1.4	n.s
GS	3	21.0	***	5	17.0	***	5	4.0	**	5	4.8	***	8	3.4	***	7	1.6	n.s
IOA	3	7.0	***	5	1.9	n.s	5	4.2	***	5	2.2	n.s	8	1.9	n.s	7	4.1	***
MS	3	2.8	*	5	2.9	**	5	1.9	n.s	5	1.6	n.s	8	1.5	n.s	7	0.6	n.s
Sublabialia	3	7.2	***	5	5.2	***	5	2.9	**	5	2.7	*	8	4.3	***	7	1.5	n.s
Supralabialia	3	2.0	n.s	5	10.6	***	5	11.0	***	5	7.6	***	8	9.2	***	7	10.3	***
RelAD	3	3.3	*	5	3.2	**	5	1.3	n.s	5	4.2	***	8	3.5	***	7	2.3	**
RelAOL	3	0.4	n.s	5	0.7	n.s	5	2.1	n.s	5	0.6	n.s	8	0.5	n.s	7	0.6	n.s
RelASL	3	0.7	n.s	5	3.6	**	5	3.6	**	5	4.8	***	8	4.0	***	7	2.5	**
RelHBL	3	5.8	***	5	2.4	*	5	0.9	n.s	5	2.4	*	8	1.9	n.s	7	7.8	***
RelHZB	3	4.4	**	5	0.4	n.s	5	0.1	n.s	5	1.2	n.s	8	2.0	n.s	7	2.9	**
RelHZL	3	2.2	n.s	5	0.4	n.s	5	0.9	n.s	5	2.7	*	8	2.0	n.s	7	5.2	***
RelIOB	3	2.4	n.s	5	4.3	***	5	2.3	*	5	2.0	n.s	8	3.1	**	7	0.7	n.s
RelKB	3	5.4	***	5	3.2	**	5	4.9	***	5	4.1	**	8	3.8	***	7	2.5	**
RelKH	3	1.5	n.s	5	2.0	n.s	5	3.1	**	5	2.3	n.s	8	1.6	n.s	7	2.1	*
RelKL	3	1.7	n.s	5	0.7	n.s	5	1.3	n.s	5	1.1	n.s	8	0.7	n.s	7	2.2	*
RelKRL	3	1.1	n.s	5	0.7	n.s	5	1.4	n.s	5	0.9	n.s	8	0.7	n.s	7	1.7	n.s
RelMOL	3	7.7	***	5	61.9	***	5	51.0	***	5	46.3	***	8	42.3	***	7	1.4	n.s
RelVBL	3	3.0	*	5	4.7	***	5	2.1	n.s	5	2.3	*	8	2.5	**	7	5.3	***
RelVHBL	3	0.3	n.s	5	0.3	n.s	5	3.3	**	5	0.6	n.s	8	0.6	n.s	7	2.6	**

Improving group discrimination

Two main multivariate techniques were used to investigate the population systematics of gecko *Tarentola* in North Africa.

Linear Discriminant function analysis (LDFA), run in a number of OTUs, this technique was used in order to elucidate general pattern of geographic variation; while Principle component analysis (PCA), run on individual specimens to investigate the relationships between pairs of adjoining populations. In addition, PCAs of the OTUs means of each character were run in order to test and support the results of LDFA.

2.3.1. Linear Discriminant function analysis (LDFA)

In order to determine how the groups differed and to develop a model with which to classify animals into groups, we conducted LDFA. The analyses were run on a number of OTUs. The combined groups plot ‘‘Canonical Discriminant Function’’ show the classification results, it provides a nice picture of the relationship between predicted group and two DFs. Since group membership is coded by color and shape, in this plot you can see where each animal falls in the space defined by the two discriminant functions. The classification was based on probabilities using both discriminant functions.

LDFA1[a]: The analysis runs on a portion of OTUs [*T. sp*-Tunisia, *T. deserti*-North Africa, *T. sp*-complex-Libya, and *T. deserti*-Libya] only males, (Figure.21a) specimens were plotted together.

To interpret the LDFA1[a], three discriminant functions (DFs) are obtained. The first accounts for 74.3% of the total among-groups variability; the second accounts for 19.7%; and the third for the remaining 5.9%. DF_1: separates group (*Tarentola. sp*-Tunisia and *T. deserti*-North Africa) ‘‘who score high on this function’’ from the other groups (*T. sp*-complex-Libya and *T. deserti*-Libya). DF_2: separates *T.sp*-Tunisia ‘‘who score high on this function’’ from *T. deserti*-North

Africa; and specimens from Libya (*T. sp*-complex and *T. deserti*) showed strong affinity.

LDFA1^{b}: the analysis runs on the same OTUs in LDFA1^{a}, but only females, specimens were plotted together (Figure.21b). Three DFs are obtained. The first accounts for 58.2% of the total variance; the second accounts for 23.6% and the third for the remaining 18.2%. DF_1: separates group (*T. deserti*-Libya and *T. sp*-complex-Libya) ‘‘who score high on this function’’ from the other groups (*T. deserti*-North Africa and *T. sp*-Tunisia). DF_2: separates *T. deserti*-North Africa ‘‘who score high on this function’’ from *T. sp-Tunisia*. Group *T. deserti*-Libya and *T. sp*-complex-Libya showed strong affinity, this pattern of overlap was obvious in males group, as here in females group, however there is little difference between two groups (*T. deserti*-Libya and *T. sp*-complex-Libya), and this is clear in the group centroid of the both.

LDFA2^{a}: The analysis runs on a portion of OTUs, only males [*T. mauritanica*-Tunisia, *T. m. fascicularis*-Libya, *T. deserti*-North Africa, *T. deserti*-Libya, *T. mauritanica*-Morocco, and *T. mauritanica*-Algeria], all these six groups were plotted together (Figure.22a). The first DF accounts for 81.2% of the total among-groups variability, the second accounts for 10.8%. DF_1: separates group (*T. m. fascicularis*-Libya and *T. deserti*-Libya) from the other North African group (*T. deserti*-North Africa, *T. mauritanica*-Algeria, *T. mauritanica*-Tunisia, and *T. mauritanica*-Morocco). DF_2: separates *T. deserti*-North Africa from North Africa *T. mauritanica* group (Tunisia, Algeria, and Morocco), while showing little difference between North African *T. mauritanica* group, and showing overlap between Libyan groups (*T. m. fascicularis* and *T. deserti*)

LDFA2^{b}: the analysis runs on the same OTUs in LDFA2^{a}, but only females, specimens were plotted together (Figure.22b). The first DF accounts for 54.2% of the total among-groups variability, the second accounts for 28.1%. DF_1: separates groups (*T. deserti*-North Africa, *T. mauritanica*-Algeria, *T. mauritanica*-Tunisia, and *T. mauritanica*-Morocco) from the other Libyan groups (*T. deserti*, and *T. m. fascicularis*). DF_2: shows a clear divergence between *T. deserti-North*

Africa ‘‘which have high score on both functions’’ and groups *T. mauritanica*-North Africa (Tunisia, Algeria, and Morocco); and it also shows separation between group *T. deserti-Libya* and *T. m. fascicularis*, this separation was considerably clearer in females than in males; while it shows strong affinity (overlap) between groups *T. mauritanica*-Tunisia, Algeria, and Morocco; but anyway there is little difference between them.

LDFA3[a]: The analysis runs on a segment of OTUs, only males (*T. sp*-complex-Libya, *T. deserti*-Libya and group *T. mauritanica*- from Tunisia, Algeria, and Morocco), all these five groups were plotted together (Figure.23a). The two first DFs account for 92.2% of the total among-groups variability, ‘‘the first DF accounts for 81.6%, the second accounts for 10.6%’’. DF_1: separates groups North Africa *T. mauritanica* (Tunisia, Algeria, and Morocco) from the Libyan groups (*T. sp-complex*, and *T. deserti)*. DF_2: separates *T. mauritanica*-Algeria from *T. mauritanica*- Tunisia and Morocco, and shows a kind of convergence between *T. mauritanica* Tunisia and Morocco. Despite there is affinity or overlapping between *T. deserti*-Libya and *T. sp*-complex-Libya, but there is some divergence between them, and this is clear in the mean (group centroid) of each group.

LDFA3[b]: The analysis runs on the same OTUs in LDFA3[a,] but this time only females specimens, all these groups were plotted together (Figure.23b). The two first DFs account for 87.5% of total variance between groups, the first accounts for 60.5%, and the second accounts for 27.0%. DF_1: separates Libyan geckos *T. sp*-complex and *T. deserti* from the other North African groups (*T. mauritanica* Tunisia, Algeria, and Morocco). DF_2: shows clear divergence between *T. sp-complex*-Libya and *T. deserti*-Libya, despite this pattern of divergence was considerably clearer in males than in females, but was evident in both. On the other side the North African (Tunisia, Algeria, and Morocco) *T. mauritanica* show overlapping or affinity.

LDFA4[a]: The analysis runs on a portion of OTUs, only males (*T. mauritanica*-North Africa [Tunisia, Algeria, Morocco], and Libyan specimens *T. deserti*, *T. sp*-

Ras Lanuf, *T. sp*- sister group Ras Lanuf), all these groups plotted together (Figure.24a). The two first DFs account for 93.5% of the total among-groups variability, the first accounts for 84.6%, the second accounts for 8.9%. DF_1: separates groups North African (Tunisia, Algeria, and Morocco) *T. mauritanica* from Libyan groups (*T. deserti*-Libya, *T. sp*-Ras Lanuf, and *T. sp*-sister group Ras Lanuf). DF_2: shows evident separation between *T. deserti*-Libya and groups *T. sp* Ras Lanuf and sister group Ras Lanuf. In the same time it is shows affinity between groups *T. sp* Ras Lanuf and sister group Ras Lanuf. On the other hand, we can observe there is overlapping between North African *T. mauritanica* from Tunisia and Morocco, while *T. mauritanica*-Algeria shows divergence from both *T. mauritanica* Tunisia and Morocco.

LDFA4^{b}: the analysis run on the same OTUs in LDFA4^{a}, but only females specimens, all these groups were plotted together (Figure.24b). The two first DFs account for 88.9% of total variance between groups, the first accounts for 78.1%, and the second accounts for 10.8%. DF_1: almost the same result as in the former analysis (males) was observed. DF_2: there is some difference when we compare with previous analysis; here there is overlapping between *T. deserti*-Libya and *T. sp*-Ras Lanuf, while there is divergence between these two groups (*T. deserti*-Libya and *T. sp-Ras* Lanuf) and *T. sp*-sister group Ras Lanuf. On the other side groups *T. mauritanica* North Africa showed strong affinity.

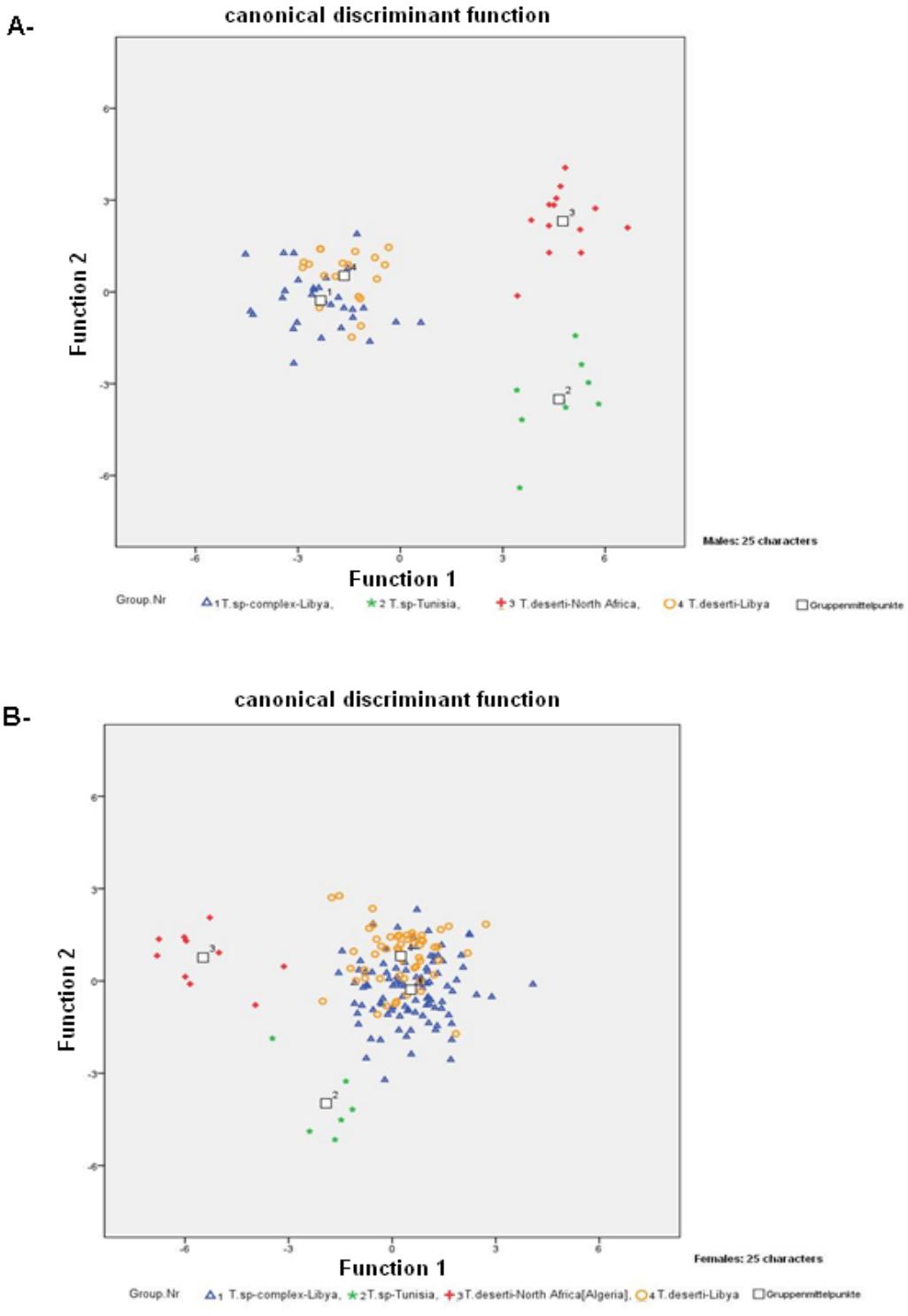


Figure 21. CDF plots for *Tarentola sp*-Tunisia, *Tarentola deserti*-North Africa, *Tarentola sp*-complex-Libya, and *Tarentola deserti*-Libya; A represents males, and B females.

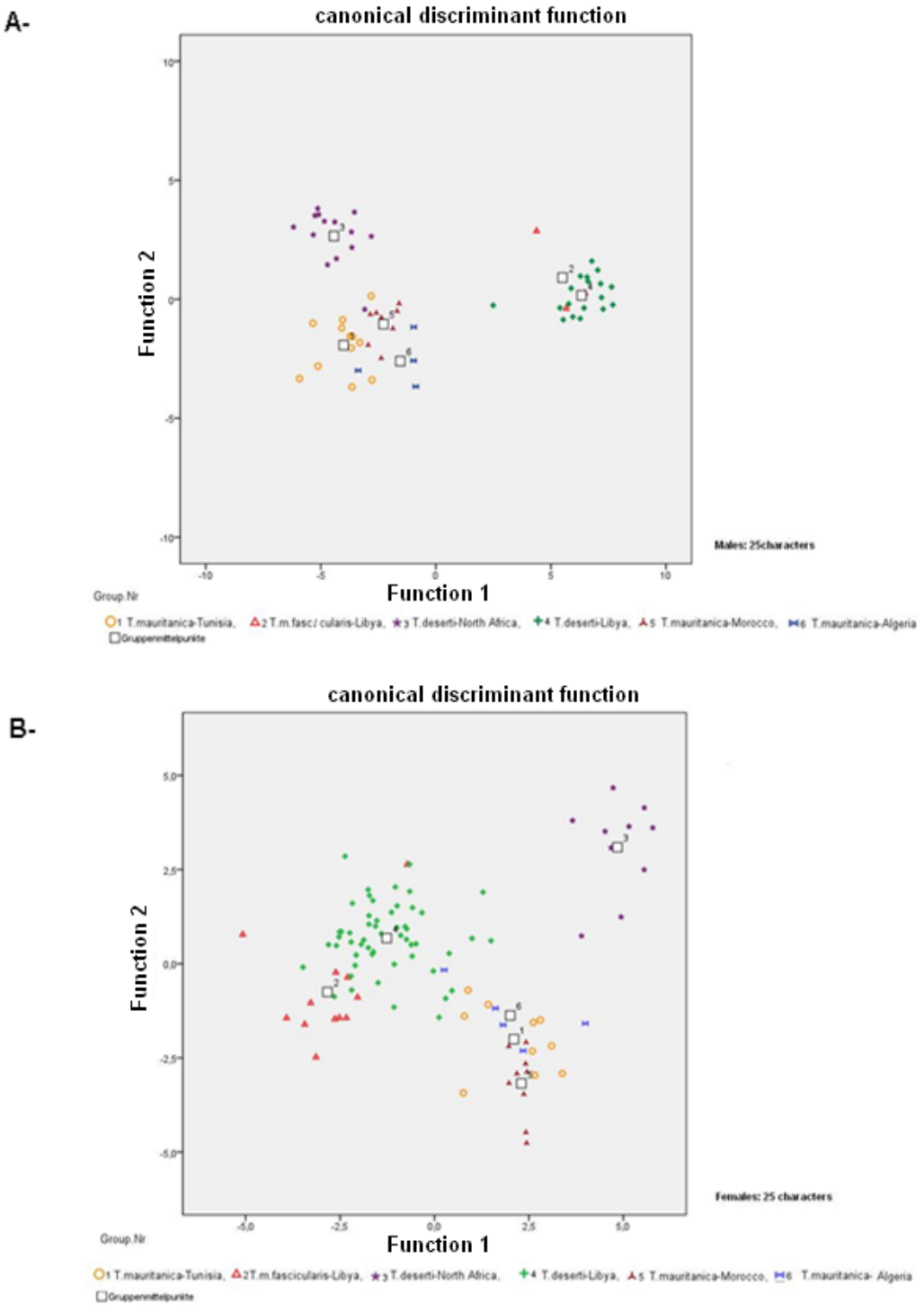


Figure 22. CDF plots for six groups of *Tarentola* (*T. mauritanica*-Tunisia, *T. m. fascicularis*-Libya, *T. deserti*-North Africa, *T. deserti*-Libya, *T. mauritanica*-Morocco, and *T. mauritanica*-Algeria; A represents males, and B females.

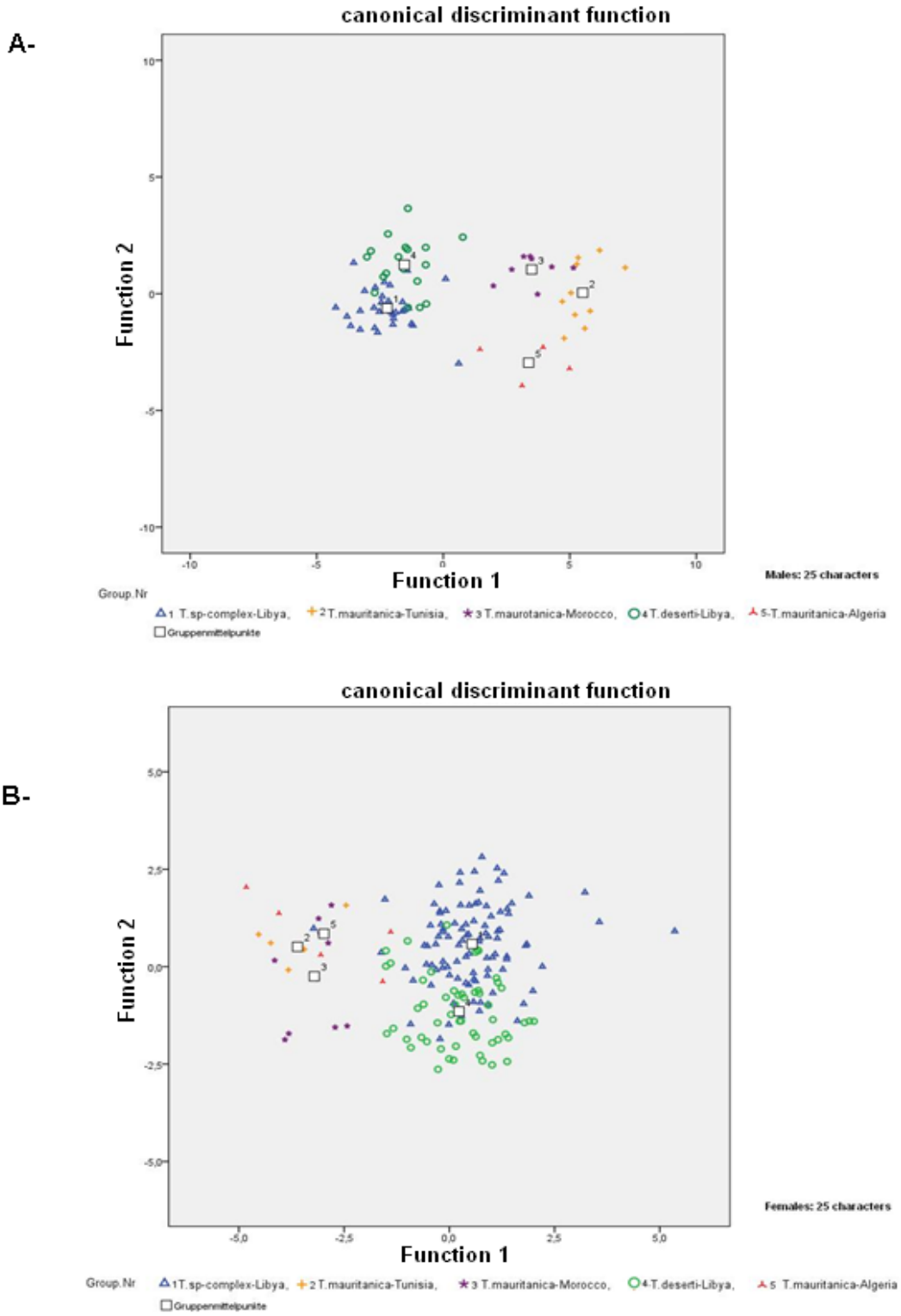


Figure 23. CDF plots for five groups of *Tarentola* (*T. sp*-complex-Libya, *T. mauritanica*- Tunisia, *T. mauritanica*-Morocco, *T. deserti*-Libya, and *T. mauritanica*-Algeria); A represent males, and B females.

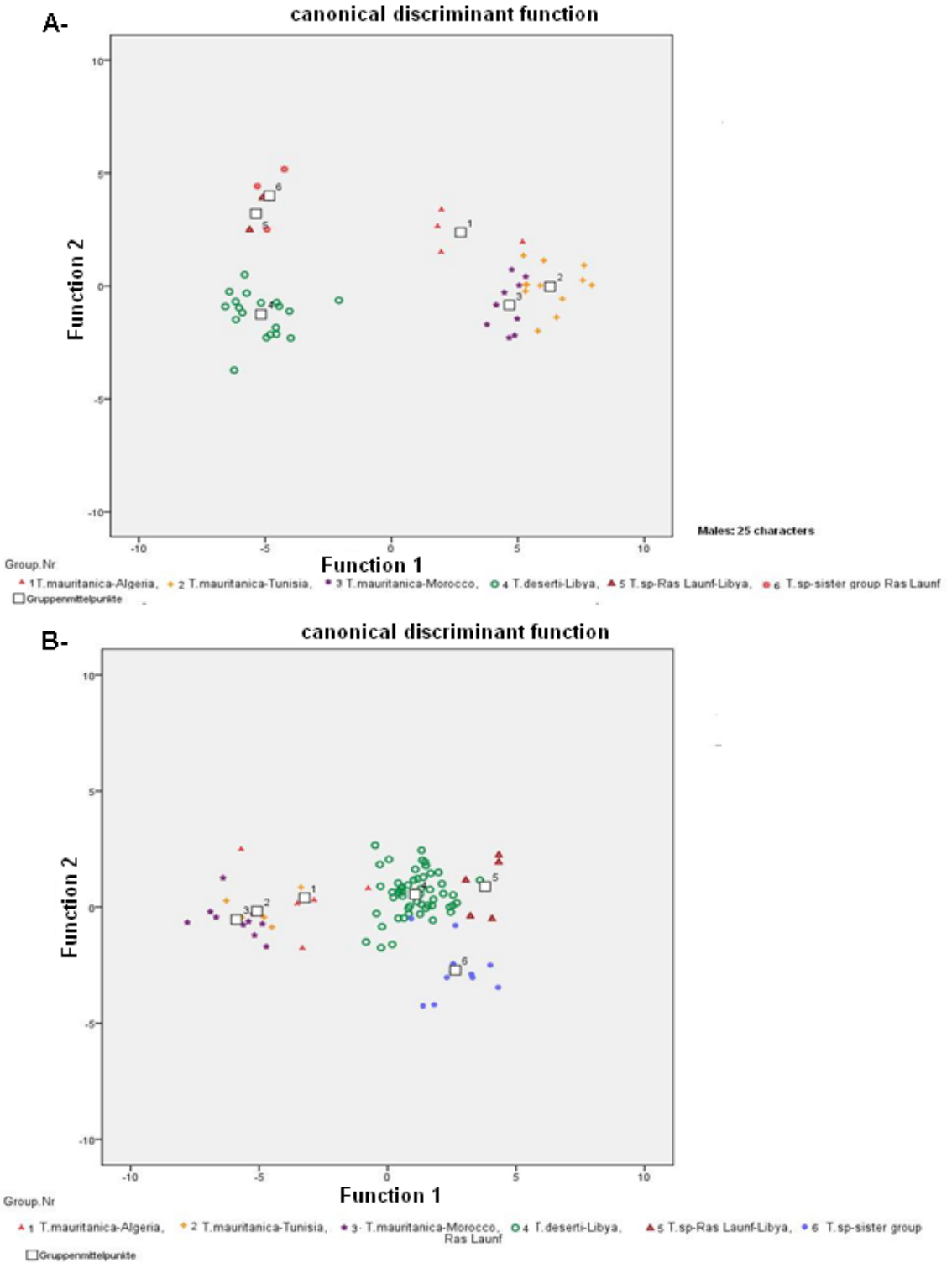


Figure 24. CDF plots for six groups of *Tarentola* (*T. mauritanica*-Algeria, *T. mauritanica*-Tunisia, *T. mauritanica*-Morocco, *T. deserti*-Libya, and *T. sp*-Ras Lanuf-Libya, and *T. sp*-sister group Ras Lanuf); A represent males, and B females.

LDFA5[a]: The analysis was run on a part of OTUs, only males (*T. sp*-Sabha-South Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Morocco, *T. deserti*-Libya, *T. mauritanica*-Algeria, and *T. sp*-Suirt-sister group. Sabha), all these six groups plotted together (Figure.25a). The two first DFs account for 89.1% of total among-groups variability (the first accounts for 75.5% and the second accounts for 13.6%). DF_1: separates *T. sp*-Sabha-South Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Morocco, and *T. mauritanica*-Algeria from *T. deserti*-Libya, and *T. sp*-Suirt-sister group Sabha. DF_2: shows clear divergence between *T. sp*-Sabha-South Libya from all remaining groups. While the group *T. mauritanica* North Africa show a kind of convergence, also group *T. deserti*-Libya and *T. sp*-Suirt sister group Sabha show a kind of affinity.

LDFA5[b]: The analysis was run on the same OTUs in LDFA5[a], but only female specimens, all six groups were plotted together (Figure.25b). The two first DFs account for 86.1% of total among-groups variability (the first accounts for 50.9% and the second accounts for 35.3%). DF_1: almost the same result as in the previous analysis (LDFA5[a]) was reached. DF_2: here also as in the former analysis, there is clear divergence between *T. sp*-Sabha-South Libya from all remaining groups, while all remaining groups show a kind of convergence.

LDFA6[a]: The analysis was run on a portion of OTUs, only males (*T. mauritanica*-Tunisia, *T. mauritanica*-Morocco, *T. sp*-Suirt-sister group Ras Lanuf, *T. deserti*-Libya, *T. mauritanica*-Algeria, *T. m. fascicularis*-Egypt, *T. m. fascicularis*-Libya, *T. mauritanica*-Tripolitania ‘‘without setting a precise site’’, and *T. sp*-Sabha-South Libya), all these groups were plotted together (Figure.26a). The two first DFs account for 80.1% of total among-groups variability (the first accounts for 69.7% and the second accounts for 10.4%). DF_1: separates between some Libyan groups (*T. deserti*, *T. m. fascicularis*, and *T. sp*-Suirt-sister group Sabha) and the remaining groups. DF_2: there is apparent separation between *T. sp*-Sabha-South Libya and the rest of groups, while there is convergence between group *T. mauritanica* from Tunisia, Algeria, Morocco, Tripolitania and

T. m. fascicularis-Egypt; also there is a kind of affinity between group *T. deserti*-Libya, *T. m. fascicularis*, and *T. sp*-Suirt-sister group Sabha.

LDFA6^{b}: The analysis was run on the same OTUs in LDFA6^{a}, but only female specimens were used, all groups were plotted together (Figure.26b). The two first DFs account for 70.0% of total among-groups variability (the first accounts for 45.2% and the second accounts for 24.7%). DF_1: shows almost the same result as in the former analysis (LDFA6^{a}) DF_2: shows the same pattern of divergence between *T. sp*-Sabha-South Libya and the rest of groups, this pattern of divergence was considerably clearer in females than in males. The rest of groups were almost the same as in the previous analysis with males.

LDFA7^{a}: The analysis was run on a portion of OTUs, only males (*T. sp*-complex-Libya, *T. sp*-Suirt-sister group Sabha, *T. deserti*-Libya, *T. sp*-Ras Lanuf-Libya, *T. sp*-sister group Ras Lanuf, *T. m. fascicularis*-Libya, *T. neglecta*-South Libya, *T. sp*-Sabha-South Libya), all these groups were plotted together (Figure.27a). The two first DFs account for 58.9% of total among-groups variability (the first accounts for 33.7% and the second accounts for 25.2%). DF_1: Shows a clear separation between the group classified as *T. neglecta*- South Libya, *T. sp*-Sabha-South Libya and of the all rest groups. DF_2: shows clear divergence between *T. neglecta*-South Libya and *T. sp*-Sabha, also these two groups are divergent from all remaining groups; on the other side, DF_2 also shows separation between *T. m. fascicularis*-Libya and all remaining groups, while there is a kind of convergence between the rest of the groups.

LDFA7^{b}: The analysis was conducted on the same OTUs in LDFA7a, but only female specimens, all groups were plotted together (Figure.27b). The two first DFs account for 57.9% of total among-groups variability (the first accounts for 35.0% and the second accounts for 22.9%). DF_1: shows nearly the same patterns of separation between groups as in the former analysis LDFA7^{a}. DF2: also demonstrates more or less the same patterns as in the previous analysis with males, but the only difference is *T. m. fascicularis*-Libya did not show the

same patterns of divergence as in males, here they show more affinity to the remaining groups.

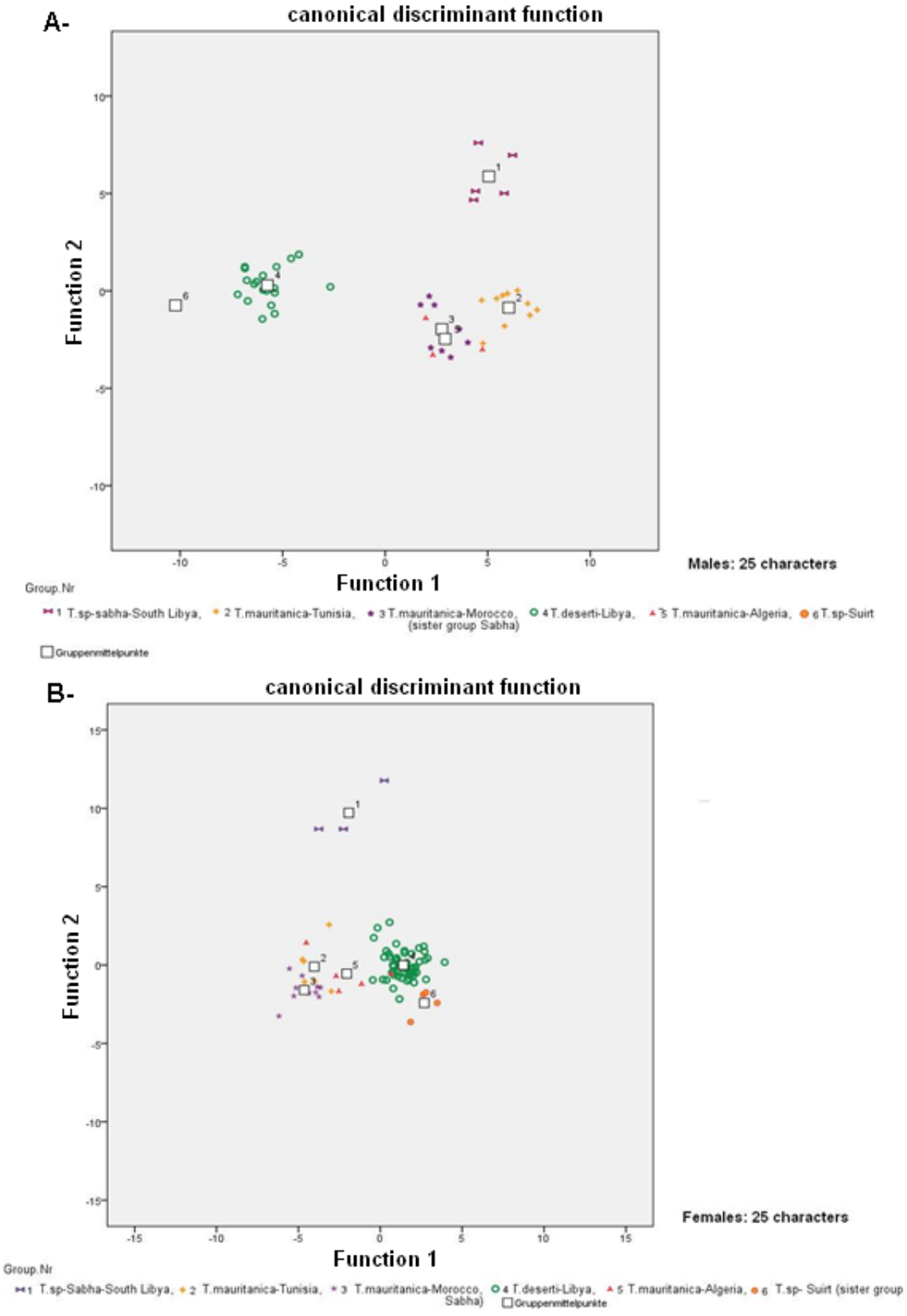


Figure 25. CDF plots for six groups of *Tarentola* (*T. sp*-Sabha-South Libya, *T. mauritanica*- Tunisia, *T. mauritanica*-Morocco, *T. deserti*-Libya, *T. mauritanica*-Algeria, and *T. sp*-Suirt-sister group Sabha); A represent males, and B females.

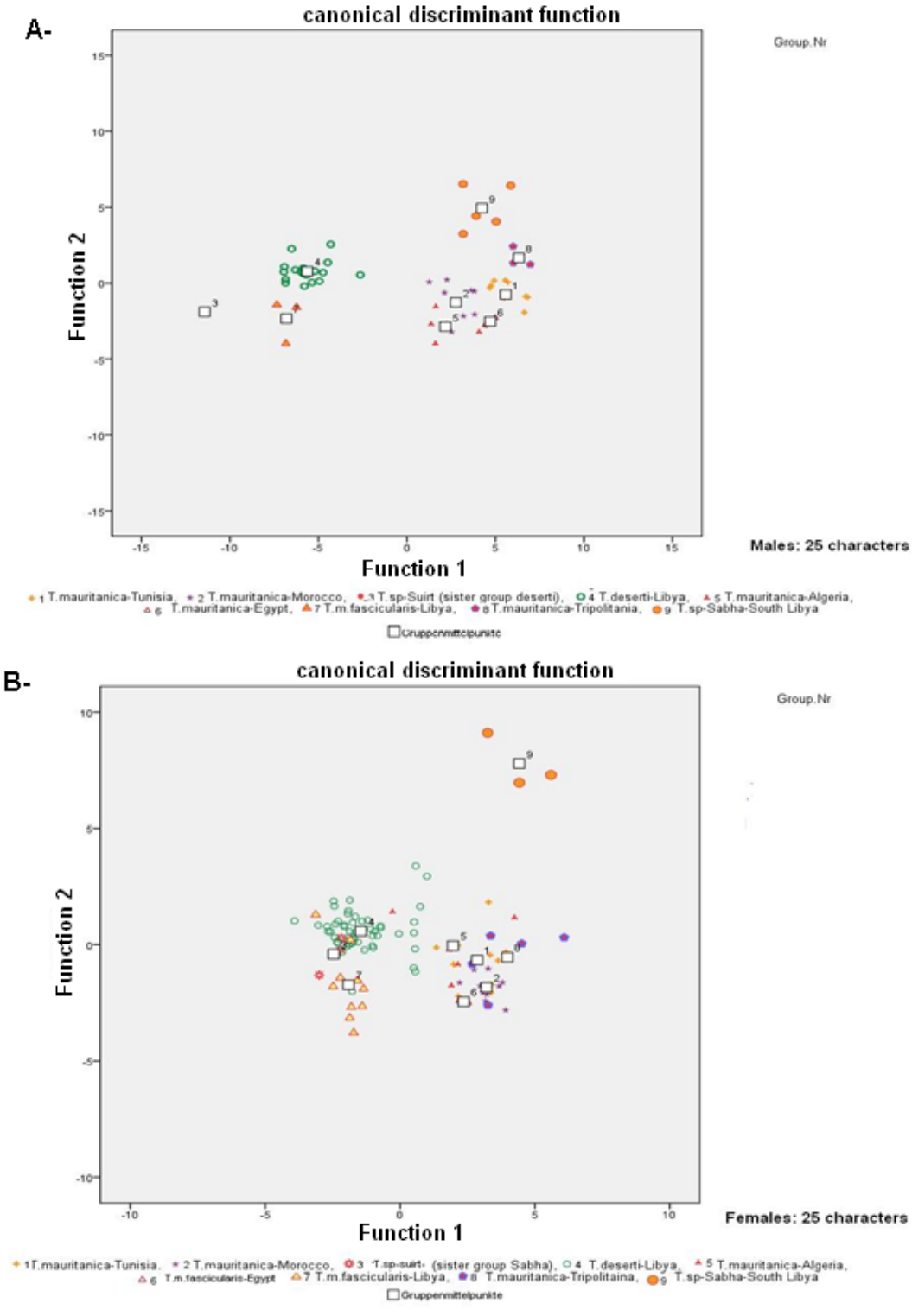


Figure 26. CDF plots for nine groups of *Tarentola* (*T. mauritanica*- Tunisia, *T. mauritanica*-Morocco, *T. sp*-Suirt-sister group Sabha, *T. deserti*-Libya, *T. mauritanica*-Algeria, *T. m. fascicularis*-Egypt, *T. m. fascicularis*-Libya, *T. mauritanica*-Tripolitania, and *T. sp*-Sabha-South Libya; A represent males, and B females

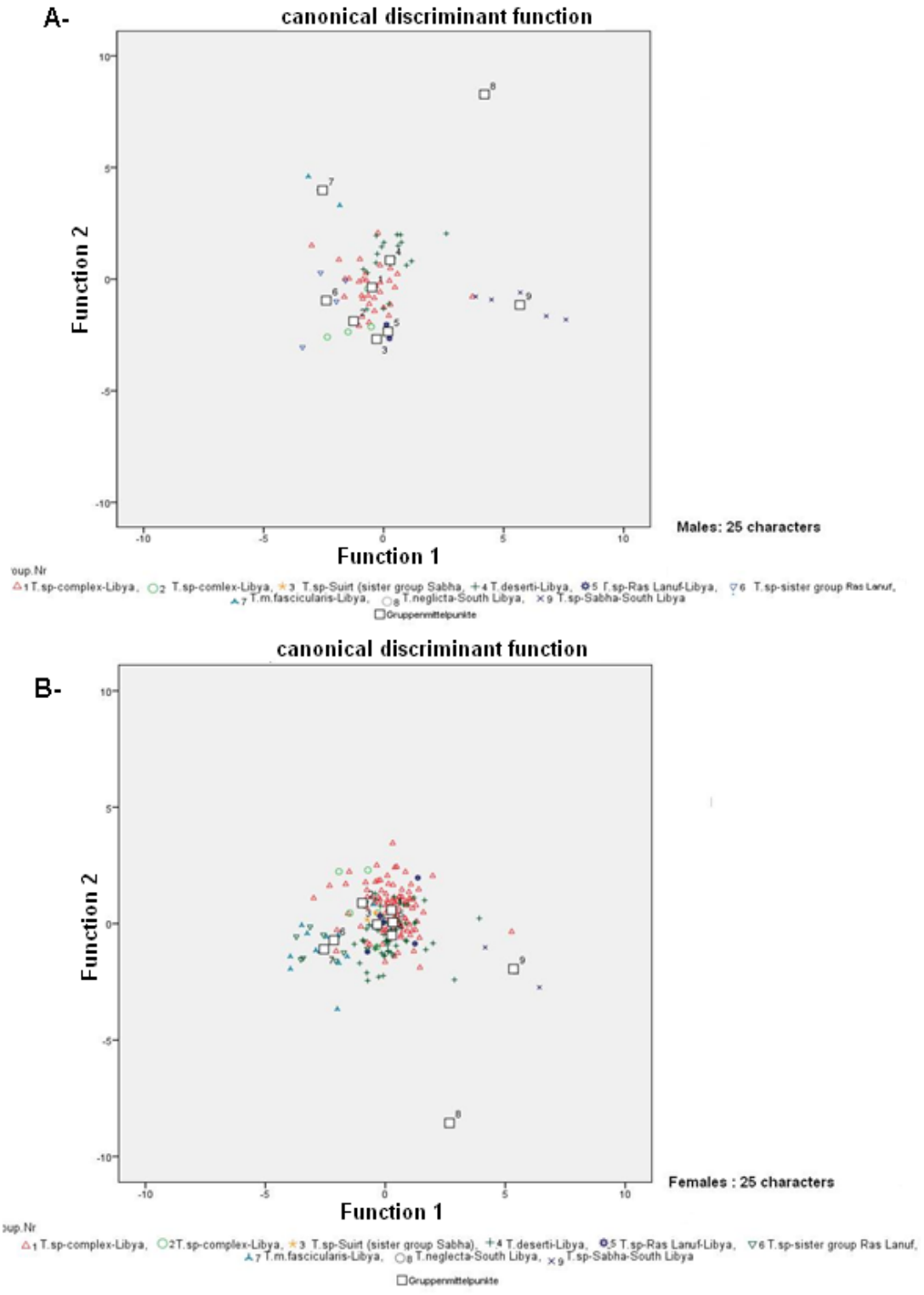


Figure 27. CDF plots for nine groups of *Tarentola* (*T. sp*-complex1-Libya, *T. sp*-complex2-Libya, *T. sp*-Suirt-sister group Sabha, *T. deserti*-Libya, *T. sp*-Ras Lanuf-Libya, *T. sp*-sister group Ras Lanuf, *T. m. fascicularis*-Libya, *T. neglecta*-South Libya, and *T. sp*-Sabha-South Libya; A represent males, and B females

2.3.2. **Principal Component Analysis**

The Initial groups used to select significant variable characters were loosely defined based on geographic proximity and phylogenetic relationships. To confirm the correctness of these grouping, The following PCAs were performed using subsets of the full range of specimens:

PCA1[a]: The groups *T. deserti*-Libya, *T. sp*-complex-Libya, *T. deserti*-North Africa, and *T. sp*-Tunisia. Only males were plotted together. The first two components for the present data account for 22.51% and 14.65% of the total variation, respectively, so that a two-dimensional plot with respect to these PCs, representing 37.16% of the variation, gives a reasonably good approximation to the relative positions of the observations in this space (Figure.28a), two eigenvectors extracted from the correlations matrix (Table 10). It was noted that, the first two PCs are successful in separating the groups (*T. deserti*-Libya, *T. sp*-complex-Libya, *and T. sp*-Tunisia) from the group *T. deserti*-North Africa,

Table 10. Factor loading for PCA, based on correlations, PCA1[a] (males group): Eigenvalue for factor 1 is 5.63 (22.51% total variance), for factor 2 is 3.66 (14.65% total variance). PCA1[b] (females group): Eigenvalue for factor 1 is 5.03 (20.11% total variance), for factor 2 is 3.50 (14.01% total variance).

Variable	Factor 1 Males group	Factor 2 Males group	Factor 1 Females group	Factor 2 Females group
RelED	0.007480	0.285346	0.105759	-0.111542
RelAOL	0.415274	-0.258246	-0.196911	-0.508352
RelASL	0.652145	-0.128220	-0.774468	-0.134404
RelHLL	0.265922	0.531184	0.121106	0.332392
RelHDW	0.233559	-0.253330	-0.325872	-0.052435
RelHDL	0.226602	0.404327	0.273647	-0.048449
RelIOB	0.771965	-0.181183	-0.695891	-0.159671
RelHWm	0.734687	-0.466176	-0.837574	-0.248908
RelHHm	0.737861	-0.483427	-0.792015	-0.369081
RelHL	-0.601281	0.579332	0.831450	0.240438
RelSVL	0.815142	-0.332621	-0.830860	-0.246694
RelMOL	0.491493	0.214311	0.118864	-0.166953
RelFLL	-0.005827	0.342873	0.172249	0.347418
RelFHLL	-0.136939	0.218981	0.351226	-0.082261
1st toe	0.614681	0.490611	-0.272537	0.551023
4th toe	0.714309	0.435958	-0.238542	0.753068
5th toe base	0.607890	0.462059	-0.291672	0.740407
VS	0.300893	0.357938	-0.320545	0.474145
Cr	0.410198	0.017827	-0.418927	0.168315
DT	-0.080032	-0.555407	-0.238534	0.163362
GS	-0.080032	-0.555407	-0.248386	0.670000
IOA	-0.075489	0.031940	0.088577	-0.131809
MS	-0.001894	0.371470	-0.168307	0.374316
Sublabialia	0.466365	0.547270	-0.380955	0.418875
Supralabialia	0.364977	0.137878	-0.163138	0.346188

The first component has a lower discriminative power, and showed affinity between the groups along the central part of the axis, there was no precise differentiation among them.

ANOVA test shows the existence of significant differences between samples in this group. *Tarentola deserti*-North Africa having a high number of gular scales (GS: 56±6.9) comparing with other samples in this group, also the characters: VS, DT, Sublabialia, ED, HLL are significantly differing among groups as revealed by ANOVA analysis, and no significant differences were identified in the number of MS scales, the length of RelHDW, RelHDL, RelFLL and RelVHBL (see Table 8 and 9). And therefore PC2 were successful in separating *T. deserti*-NW Africa, from the remaining groups, along the second component, in the positive side; while Libyan group (*T. deserti*-Libya, *T. sp*-complex-Libya), and *T. sp*-Tunisia shows an extensive overlapping or affinity. Almost the same patterns were observed in **PCA1[b]** (the same groups in PCA[1a], but only female specimens (Figure 28b).

PCA2[a]: The following groups were plotted together, only males, *T. deserti*-North Africa, *T. deserti*-Libya, *T. m. fascicularis*-Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco; the first component accounts for 22.06% of the total variance; the second, 17.48% (Figure.29a), two eigenvectors extracted from the correlations matrix (Table 11). The first component has a lower discriminative power, and showed overlap between the six groups in the central part of the axis. The second component has more discriminative power than the first one, and shows a clear divergence between group *T. deserti*-North Africa from (*T. deserti*-Libya, *T. m. fascicularis*-Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco), group N-African *T. deserti* set at the extreme positive part of the factor, into the direction of high values of size and scales. Six external morphological characters showed significant differences among groups as revealed by an ANOVA analysis (see Table 8 and 9), *Tarentola deserti*-NW-Africa having a large size (HLL and

FLL are: 43.1 mm, 32.3 mm respectively), also high number of gular scales, ventral scales and sublibialia scales, comparing with the remaining groups; while it was noted that, there is overlap between Libyan groups and North African *T. mauritanica* in the central part of this factor.

Table 11. Factor loading for PCA, based on correlations, PCA2[a] (males group): Eigenvalue for factor 1 is 5.55 (22.06% total variance), for factor 2 is 4.37 (17.48% total variance). PCA2[b] (females group): Eigenvalue for factor 1 is 5.58 (21.47% total variance), for factor 2 is 4.08 (16.08% total variance).

Variable	Factor 1 Males group	Factor 2 Males group	Factor 1 Females group	Factor 2 Females group
RelED	-0.070714	0.422580	0.014030	-0.055684
RelAOL	0.773664	-0.287164	-0.766543	-0.245486
RelASL	0.648071	-0.082463	-0.843094	0.085341
RelHLL	-0.063576	0.771200	0.072336	0.455390
RelHDW	0.073295	-0.172483	-0.528727	-0.218153
RelHDL	0.126842	0.564459	0.112844	-0.113898
RelIOB	0.776883	-0.086704	-0.848953	0.132163
RelHWm	0.599690	-0.228543	-0.774783	-0.207742
RelHHm	0.650938	-0.213241	-0.835713	-0.320604
RelHL	-0.541399	0.663304	0.796193	0.271528
RelSVL	0.800714	-0.401286	-0.793020	-0.270086
RelMOL	0.588922	-0.008708	-0.180301	0.191620
RelFLL	-0.187396	0.643177	-0.063551	0.205675
RelFHLL	-0.231369	0.381487	0.497598	0.140704
1st toe	0.598952	0.561087	-0.275233	0.766481
4th toe	0.685533	0.403245	-0.170848	0.799840
5th toe base	0.621001	0.538140	-0.205959	0.796614
VS	0.083031	0.406541	-0.174503	0.501619
Cr	0.389693	0.115267	-0.241968	0.020181
DT	-0.280726	-0.551084	0.054113	0.013896
GS	-0.280726	-0.551084	-0.139962	0.732469
IOA	-0.059296	-0.066295	0.012069	0.045491
MS	-0.050217	0.250513	-0.158330	0.348087
Sublabialia	0.335063	0.513459	-0.319697	0.545856
Supralabialia	0.317875	0.110027	-0.166503	0.512858

In **PCA2[b]:** Only female specimens, the same patterns of divergence and affinity were observed (Figure.29b).

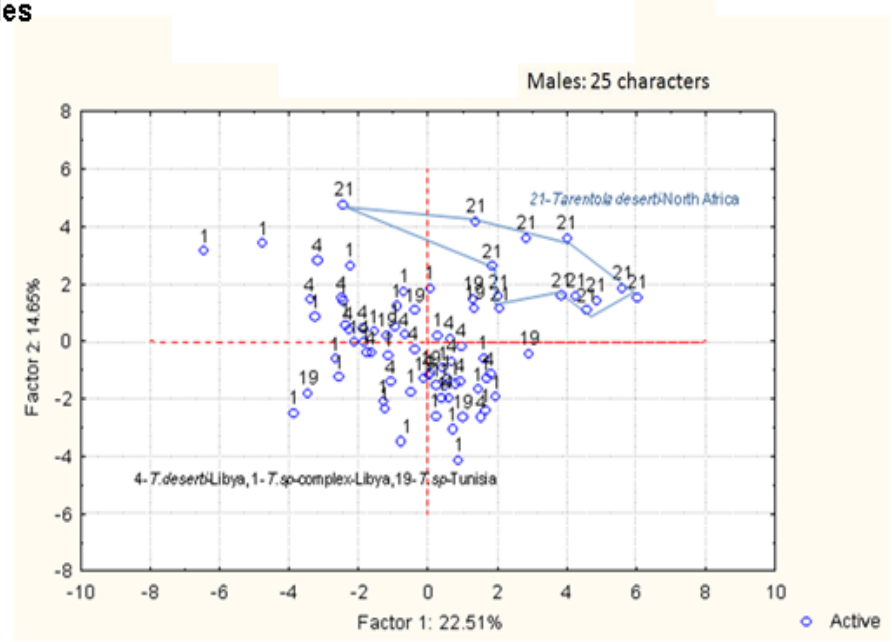
PCA3[a]: A plot of the six groups, only male specimens (*T. deserti*-Libya, *T. sp*-Ras Lanuf, *T. sp*-sister group Ras Lanuf, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco). Two eigenvectors extracted from the correlations matrix (Table 12), with respect to the first two PCs, this two-dimensional display represents 36.2% of the total variation (Figure.30a). The PCA plots indicate that there is a little difference between any of these groups,

and there is overlapping between all of them. However, PC2 can show a kind of divergence between *T. sp*-Ras Lanuf from the rest of groups, in the positive side, some of characters showed significant differences among groups as revealed by an ANOVA analysis (see Table 8 and 9), *T. sp*-Ras Lanuf have a higher number of gular scales 42-55 comparing with other groups in this analysis. Also these patterns were observed in **PCA3^{b}** (females, Figure.30b), but here the divergence between *T. sp*-Ras Lanuf from the remaining groups is more obvious than in males (PCA3^{a}), while the remaining groups show more an extensive overlapping in the central part of the first component.

Table 12. Factor loading for PCA, based on correlations, PCA3^{a} (males group): Eigenvalue for factor 1 is 5.61 (22.43% total variance), for factor 2 is 3.44 (13.77% total variance). PCA3^{b} (females group): Eigenvalue for factor 1 is 5.31 (21.23% total variance), for factor 2 is 4.59 (18.38% total variance).

Variable	Factor 1 Males group	Factor 2 Males group	Factor 1 Females group	Factor 2 Females group
RelED	-0.339567	-0.110694	-0.370844	-0.164142
RelAOL	0.809879	0.125854	-0.189818	0.771897
RelASL	0.690445	0.167261	-0.102821	0.870160
RelHLL	-0.463316	0.814868	0.931075	0.151722
RelHDW	0.374118	0.518326	0.508580	0.503081
RelHDL	-0.182873	0.473528	0.804943	0.180968
RelIOB	0.729468	0.165927	-0.078281	0.889030
RelHWm	0.593019	0.503426	-0.101162	0.822444
RelHHm	0.607243	0.240020	-0.187300	0.838589
RelHL	-0.723946	0.514242	0.958328	-0.093260
RelSVL	0.890655	-0.157730	-0.824259	-0.216407
RelMOL	0.523271	-0.091381	-0.334803	-0.039926
RelFLL	-0.499232	0.685079	0.888188	0.180371
RelFHLL	-0.370083	0.436111	0.588382	-0.419796
1st toe	0.331037	0.428531	-0.377015	0.246097
4th toe	0.533290	0.274882	-0.342076	0.260376
5th toe base	0.382940	0.457779	0.045582	0.273505
VS	-0.161773	0.221221	0.060291	0.088270
Cr	0.232738	0.077814	-0.036346	0.151934
DT	0.230924	0.240798	0.130150	0.265927
GS	0.230924	0.240798	0.092501	0.150811
IOA	0.009331	-0.263661	0.308706	-0.101556
MS	-0.020690	0.334880	-0.078125	0.032238
Sublabialia	-0.033801	-0.070544	0.242059	0.348614
Supralabialia	0.110988	-0.327942	-0.029311	0.098009

A. Males



B. Females

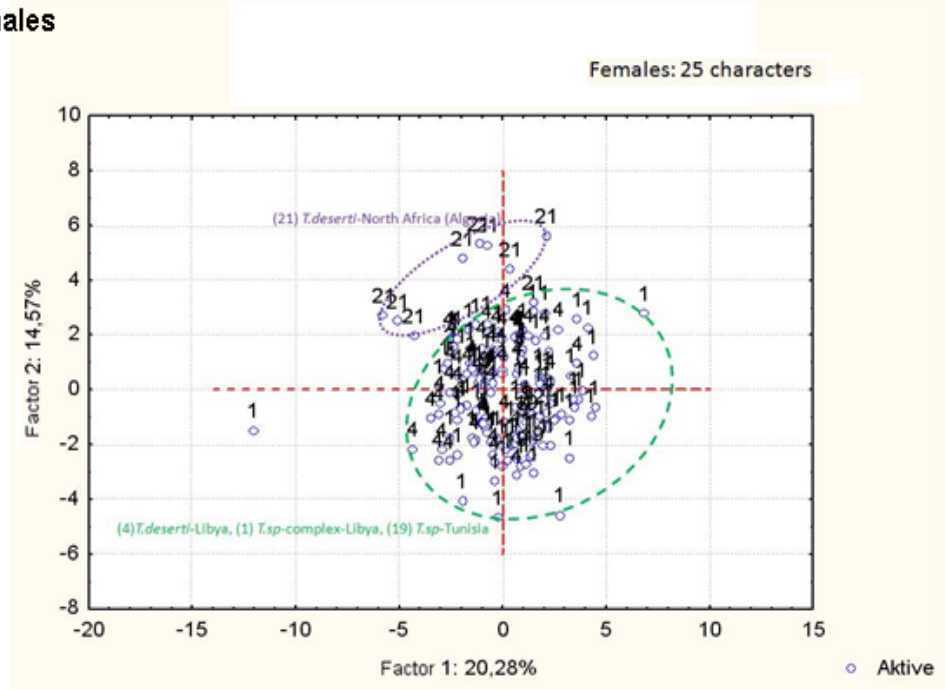
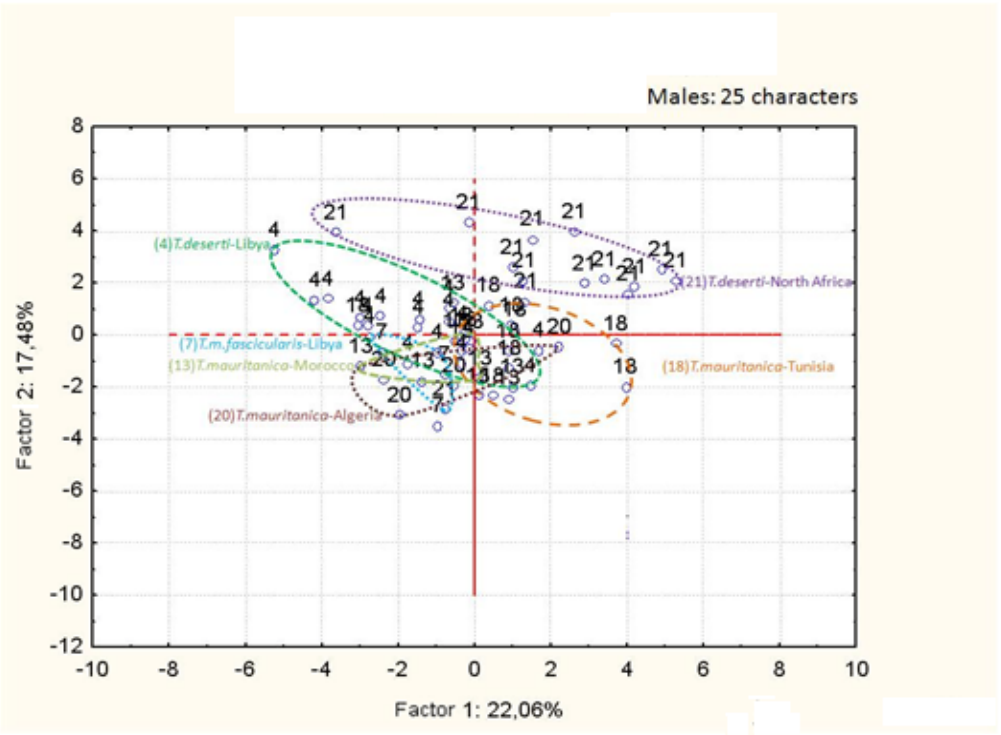


Figure 28. PCA for specimens *T. deserti*-Libya, *T. sp*-complex-Libya, *T. sp*-Tunisia, and *T. deserti*-North Africa. The first and second principal components cover 40.94% of total variance in males, and 34.85% in females.

- **Note:** These ellipses were drawn around the points with one of the drawing programs (Paint) in order to identify each group

A. males



B. Females

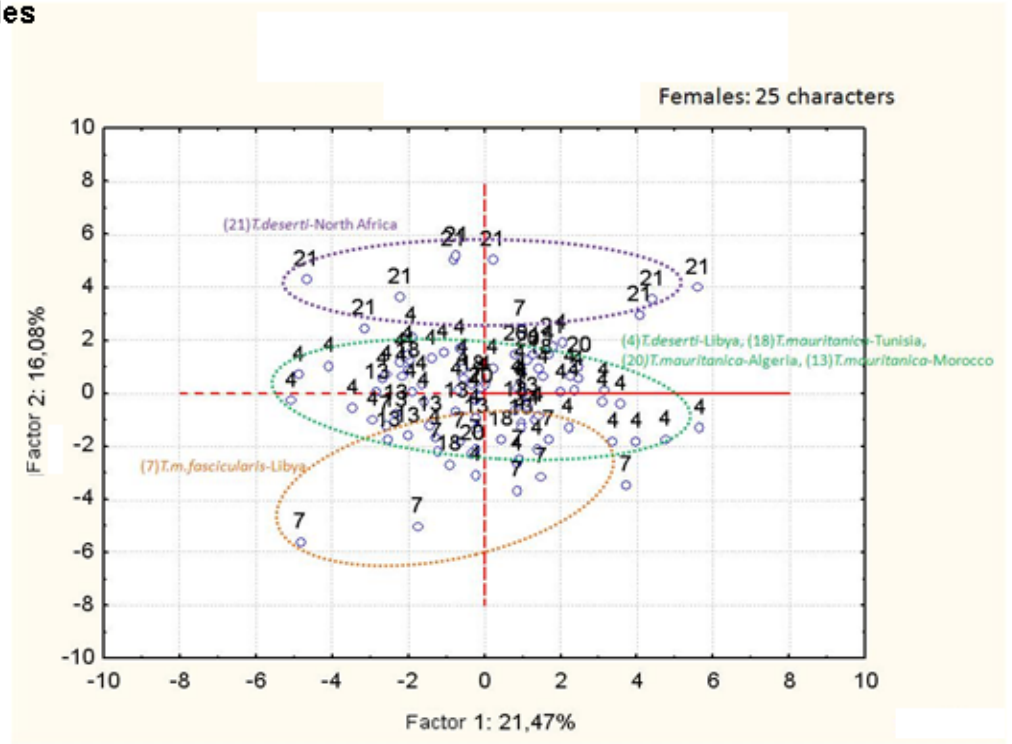
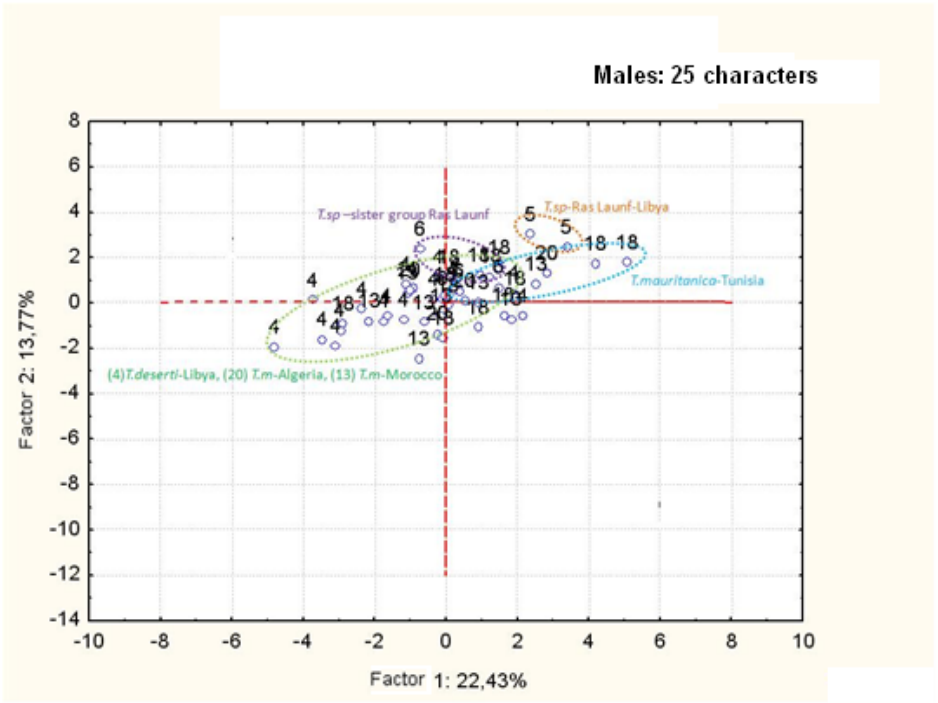


Figure 29. PCA for specimens *T. deserti*-North Africa, *T. deserti*-Libya *T. m. fascicularis*-Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco. The first and second principal components cover 39.54% of total variance in males. and 37.55% in females.

A. males



B. Females

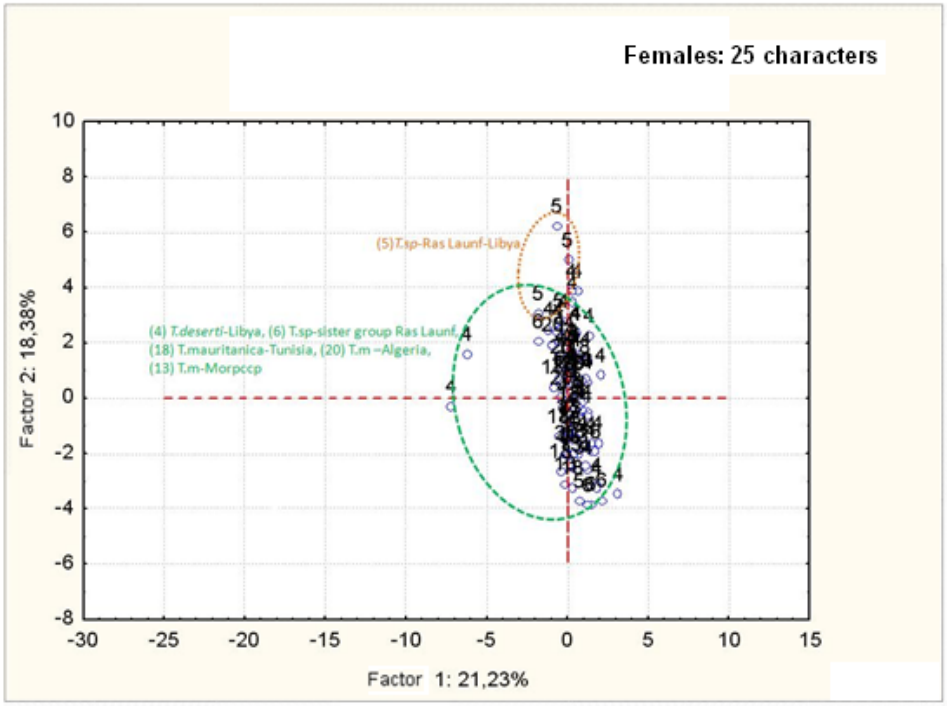


Figure 30. PCA for specimens *T. deserti*-Libya, *T. sp*-Ras Lanuf-Libya, *T. sp*-sister group Ras Lanuf-Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco. The first and second principal components cover 36.2% of total variance in males, and 40.03% in females.

PCA4[a]: Six OTUs were used in this analysis, only male specimens of (*T. deserti*-Libya, *T. sp*-Suirt [sister group Sabha], *T. sp*-Sabha-South Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco). Two eigenvectors extracted from the correlations matrix (Table 13), the first two PCs represent 44.79% of the total variability (Figure.31a). The positions of observations in two-dimensional space show, the first component is successful in separation between *T. sp*-Sabha and the remaining groups, in the negative side. Some of meristic characters showed significant differences among groups as revealed by an ANOVA analysis (see Table 8 and 9), the group *T. sp*-Sabha (South Libya) is characterized by having higher number of lamellae underneath of the first and fourth toe: 12-14, 17-19 respectively, higher number of supralabialia scales: 9-10, and MS scales: 3-5 than the other groups in the analysis, which are situated on the opposite central side of the axis. At the same time, the second component shows a kind of overlapping between group *T. deserti*-Libya and *T. sp*- Suirt with North African *T. mauritanica*. However, here we can distinguish the patterns of divergence between Libyan group (*T. deserti*, and *T. sp*-Suirt), and North African *T. mauritanica*.

In **PCA4[b]:** Only female specimens (Figure.31b), do not reveal a very clear pattern of geographic variation between the groups, here there is a strong affinity between the groups, the only exception is *T. sp*-Sabha-South Libya, this group shows clear divergence from the remaining groups.

Table 13. Factor loading for PCA, based on correlations, PCA4[a] (males group): Eigenvalue for factor 1 is 8.18 (32.72% total variance), for factor 2 is 3.02 (12.07% total variance). PCA4[b] (females group): Eigenvalue for factor 1 is 6.32 (25.28% total variance), for factor 2 is 4.10 (16.55% total variance).

Variable	Factor 1 Males group	Factor 2 Males group	Factor 1 Females group	Factor 2 Females group
RelED	-0.025917	0.549845	-0.523513	-0.252615
RelAOL	-0.610339	-0.508424	0.187820	-0.819057
RelASL	-0.557912	-0.449031	0.319934	-0.766636
RelHLL	0.841157	-0.352461	0.935636	0.177001
RelHDW	0.297361	-0.742705	0.778993	-0.297482
RelHDL	0.650839	-0.498890	0.875082	0.084156
RelIOB	-0.707848	-0.351925	0.313023	-0.807456
RelHWm	-0.498481	-0.508121	0.353900	-0.744688
RelHHm	-0.621684	-0.168986	0.191565	-0.858493
RelHL	0.914008	-0.237943	0.911360	0.331625
RelSVL	-0.918051	-0.120327	-0.650242	-0.075095
RelMOL	-0.576878	-0.428807	-0.347024	-0.193292
RelFLL	0.830318	-0.242897	0.921085	0.127617
RelFHLL	0.578068	-0.140833	0.580212	0.517816
1st toe	-0.701816	0.197946	-0.508500	-0.195129
4th toe	-0.666563	-0.051062	-0.490557	0.003942
5th toe base	-0.607241	-0.008045	-0.144108	0.148651
VS	-0.269084	0.414369	-0.035667	0.182936
Cr	-0.367835	0.015246	-0.094847	-0.178232
DT	-0.316151	-0.359957	0.126586	0.016287
GS	-0.316151	-0.359957	-0.001239	0.241712
IOA	0.045577	-0.039279	0.268955	0.266201
MS	-0.190628	-0.069271	-0.061207	-0.000785
Sublabialia	0.021178	0.042593	0.392922	-0.090367
Supralabialia	-0.594129	0.323299	-0.253171	0.079677

PCA5[a]: Nine OTUs of different species of *Tarentola* (Libyan group: *T. deserti, T. m. fascicularis, T. mauritanica*-Tripolitania ‘‘without setting a precise site’’*, T. sp*-Sabha, *T. sp*-Suirt-sister group Sabha*;* and North African group: *T. m. fascicularis*-Egypt, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, *T. mauritanica*-Morocco)*,* only males were plotted together. Two eigenvectors extracted from the correlations matrix (Table 14), the analysis distributes the male samples on a plane defined by the two first axes which covers 42.64% of the total variability (Figure.32a). First component (accounts for 31.29% of total variance), this component separates two groups: one that includes *T. sp*-Sabha and another one with all remaining groups. The group *T. sp*-Sabha appears on the negative side, the remaining populations appear widespread along the central of the axes. At least five meristic characters showed significant differences among species as revealed by an ANOVA analysis (see Table 8 and 9), the group *T. sp*-Sabha is characterized by having higher values of: ventral

scales, supralabial scales, lamellae underneath of the first, fourth and fifth toe, than the remaining groups in the analysis, it was: 40-43, 9-10, 12-14, 17-19, 21-23 respectively; they also have higher length of FLL: 26.8 mm, these characters influencing the separation of *T. sp*-sabha from other groups along the first component. Second component (accounts for 11.35% of total variance) has a lower discriminative power, but separates groups *T. mauritanica* (North Africa: Tunisia, Algeria, and Morocco) and *T. m. fascicularis*-Libya from the remaining groups.

Table 14. Factor loading for PCA, based on correlations, PCA5[a] (males group): Eigenvalue for factor 1 is 7.82 (31.29% total variance), for factor 2 is 2.84 (11.35% total variance). PCA5[b] (females group): Eigenvalue for factor 1 is 5.69 (23.22% total variance), for factor 2 is 4.17 (16.71% total variance).

Variable	Factor 1 Males group	Factor 2 Males group	Factor 1 Females group	Factor 2 Females group
RelED	-0.075772	0.641631	-0.268231	-0.079739
RelAOL	-0.533719	-0.307890	0.224429	0.721341
RelASL	-0.587397	-0.158274	0.254766	0.843289
RelHLL	0.808834	-0.191574	0.870193	-0.052828
RelHDW	0.321515	-0.708409	0.617259	0.421173
RelHDL	0.697514	-0.319241	0.807405	-0.075005
RelIOB	-0.649565	-0.135720	0.242972	0.843370
RelHWm	-0.462159	-0.545359	0.314636	0.720766
RelHHm	-0.535603	-0.141954	0.193981	0.792262
RelHL	0.909330	-0.210048	0.859107	-0.280732
RelSVL	-0.926959	-0.041889	-0.910864	0.088864
RelMOL	-0.550912	-0.154488	-0.289145	0.047776
RelFLL	0.833046	-0.211078	0.855128	0.006346
RelFHLL	0.584356	-0.187881	0.426934	-0.491697
1st toe	-0.617339	0.102504	-0.492826	0.367558
4th toe	-0.677533	-0.078332	-0.517532	0.268675
5th toe base	-0.550349	-0.133637	-0.383768	0.291265
VS	-0.280872	0.053888	-0.200564	0.225802
Cr	-0.442830	-0.052001	-0.030083	0.197129
DT	-0.315349	-0.698893	-0.101455	-0.014322
GS	-0.315349	-0.698893	-0.177424	0.168931
IOA	-0.107038	-0.095483	-0.031760	-0.013903
MS	-0.108168	-0.115415	-0.123297	0.197276
Sublabialia	0.036079	0.140474	0.013690	0.291596
Supralabialia	-0.595726	0.346842	-0.446291	0.145451

In **PCA5b:** Only females (Figure.32b), as in the males analysis, the first component have the same patterns of divergence between group *T. sp*-Sabha and the remaining groups as in males analysis. The second component has a lower discriminative power; this component shows a strong affinity between the groups.

PCA6[a]: Nine OTUs of Libyan *Tarentola* populations, only males (*T. deserti*, *T. m. fascicularis*, *T. sp*-complex1 and 2, *T. sp*-Ras Lanuf, *T. sp*-sister group Ras Lanuf, *T. sp*-Suirt, *T. sp*-Sabha, *and T. neglecta*- Gaber-Aown Oasis Lake) were plotted together. Two eigenvectors extracted from the correlations matrix (Table 15), the analysis distributes the samples on a plane defined by the two first axes which covers 43.49% of the total variability (Figure.33a). The first component was successful in separating groups *T. sp*-Sabha and *T. neglecta* from the remaining groups; the populations of *T. sp*-Sabha and *T. neglecta* appear on the negative side of the axes. ANOVA test shows the existence of significant differences among different groups in this analysis (see Table 8 and 9). *T. sp*-Sabha and *T. neglecta* having higher number of ventral scales: 40-43, 42-43 respectively, this character influencing the separation of these two groups from the remaining groups along the first component, in the negative side. Also *T. sp*-Sabha having higher number of lamellae underneath of the 1st toe and 4th toe: 12-14, 17-19 respectively, it has a high value of MOL distance: 16.3-19.1 mm; all these characters contribute in the separation of *T. sp*-Sabha from the rest groups (with the exception of *T. neglecta*) along the first axis, in the negative side.

The second component was successful in separating groups: 1- *T. sp*-Sabha from *T. neglecta*; and 2- *T. sp*-Ras Lanuf from groups (*T. deserti*-Libya, *T. m. fascicularis*, *T. sp*-complex-Libya, *and T. sp*-Suirt); in the first case, *T. neglecta* having very slim head, HW: 5.6, and 18 lamellae underneath of the fifth toe, these characters influencing the separation of *T. neglecta*-south Libya from the remaining groups in this analysis along the second axis (factor), in the negative side. In the second case, *T. sp*-Ras Lanuf having higher number of scales under the 5th toe: 22-23, with the exception of *T. sp*-Suirt which has more or less the same number; *T. sp*-Ras Lanuf has a broad head: 15.8-21.6 mm; these characters influencing the separation of *T. sp*-Ras Lanuf from all other groups along the second factor, in the positive side.

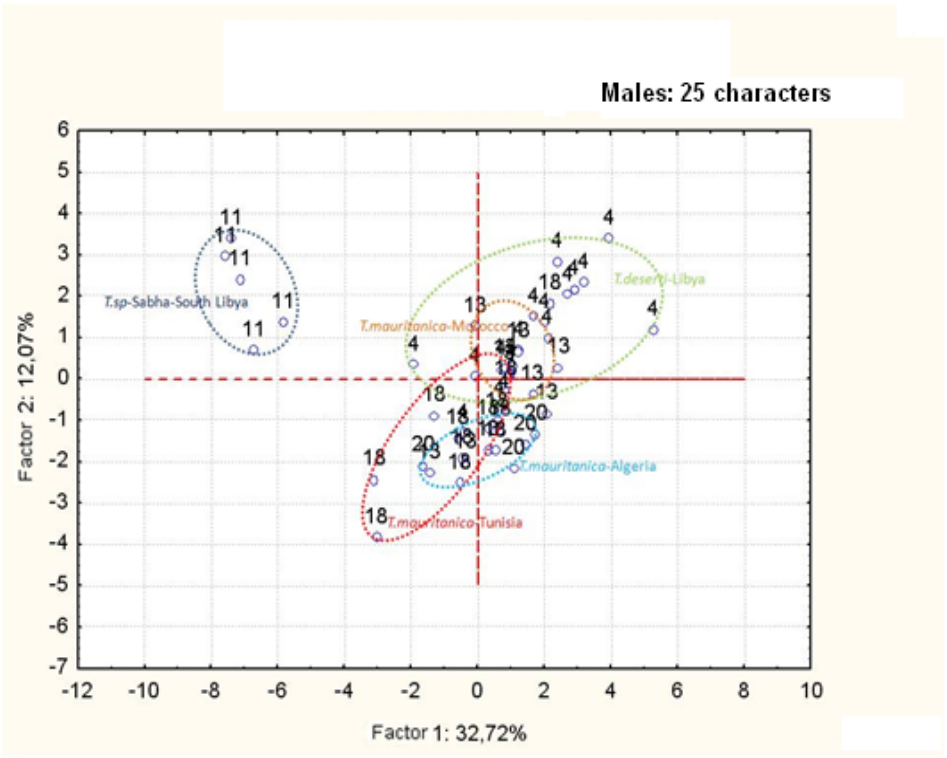
In **PCA6[b]:** Only females (Figure.33b). The first component shows a clear divergence between groups *T. sp*-Sabha and all remaining groups. The

second component has a lower discriminative power; this component shows a strong affinity between the groups.

Table 15. Factor loading for PCA, based on correlations, PCA6[a] (males group): Eigenvalue for factor 1 is 7.40 (29.59% total variance), for factor 2 is 3.47 (13.90% total variance). PCA6[b] (females group): Eigenvalue for factor 1 is 4.62 (18.49% total variance), for factor 2 is 3.86 (15.43% total variance).

Variable	Factor 1 Males group	Factor 2 Males group	Factor 1 Females group	Factor 2 Females group
RelED	-0.194772	-0.263133	-0.121580	0.194174
RelAOL	-0.230502	0.282033	0.094247	-0.415649
RelASL	-0.543434	0.311011	-0.163619	-0.834290
RelHLL	0.794216	0.529157	0.803629	-0.328815
RelHDW	0.396322	0.697099	0.537174	-0.579218
RelHDL	0.718878	0.327796	0.802901	-0.210277
RelIOB	-0.657408	0.458694	-0.092759	-0.851080
RelHWm	-0.327640	0.774025	-0.226359	-0.766688
RelHHm	-0.644581	0.498179	-0.281771	-0.755195
RelHL	0.938640	0.211688	0.881578	-0.038497
RelSVL	-0.915650	0.096323	-0.550988	0.258000
RelMOL	-0.757260	-0.103243	-0.032017	0.010116
RelFLL	0.806314	0.476935	0.513054	-0.271572
RelFHLL	0.587966	0.328747	0.641787	0.092613
1st toe	-0.457368	0.111301	-0.512573	-0.074251
4th toe	-0.573792	0.286942	-0.522420	-0.211346
5th toe base	-0.291391	0.381023	-0.310595	-0.300682
VS	-0.334110	0.092002	-0.383598	-0.152122
Cr	-0.292822	0.231684	-0.127816	-0.201582
DT	-0.362535	0.508464	-0.085769	-0.192598
GS	-0.362535	0.508464	-0.275790	-0.207461
IOA	0.068997	-0.030968	0.197997	0.051736
MS	0.083419	0.101688	-0.178780	-0.085304
Sublabialia	0.007215	-0.080709	-0.101606	-0.369208
Supralabialia	-0.605081	-0.245232	-0.370693	0.003243

A. males



B. Females

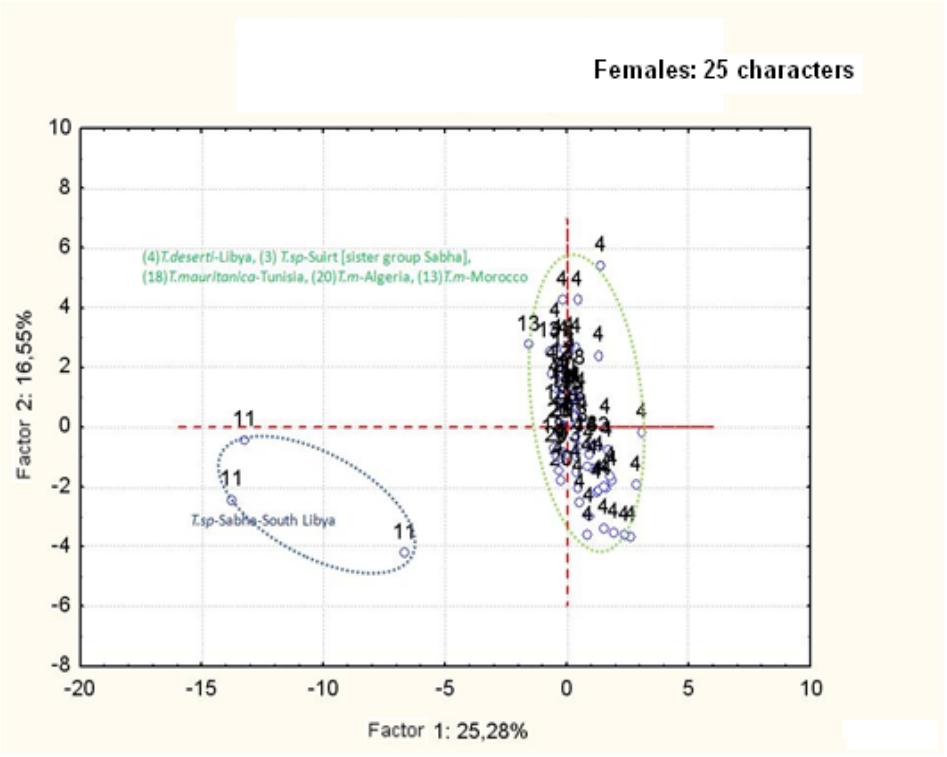
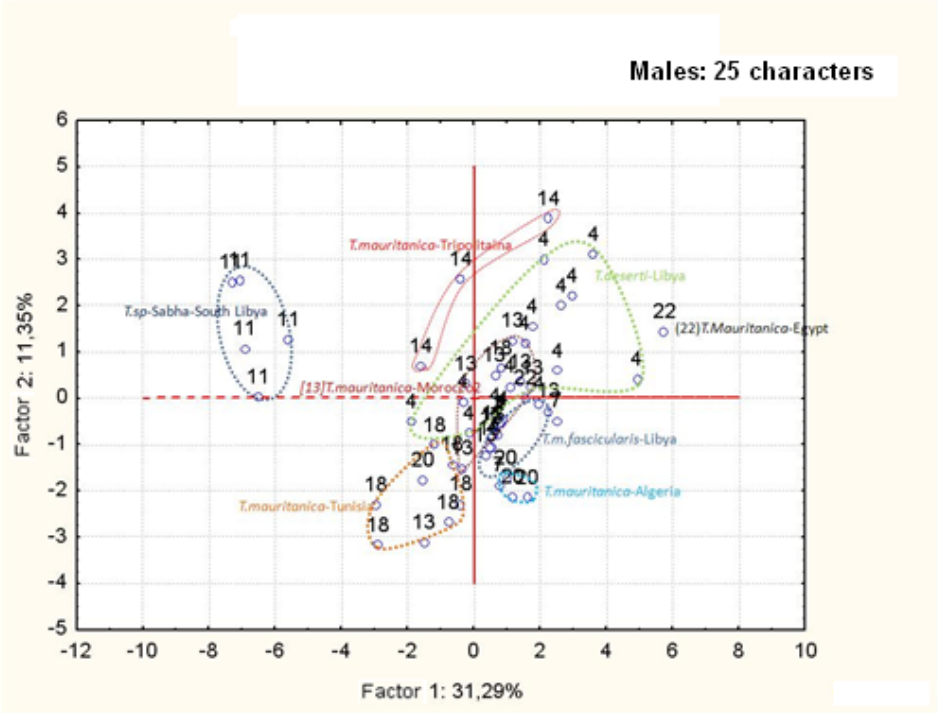


Figure 31. PCA for specimens *T. deserti*-Libya, *T. sp*-Suirt-Libya, *T. sp*-Sabha-South Libya, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco. The first and second principal components cover 44.79% of total variance in males, and 41.83% in females.

A. males



B. Females

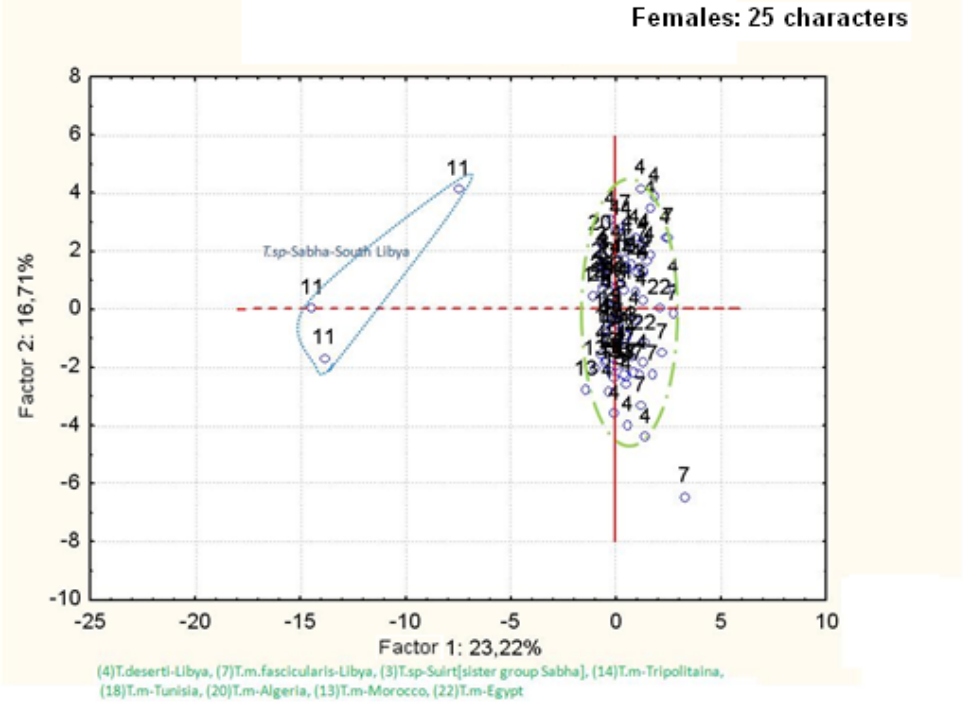
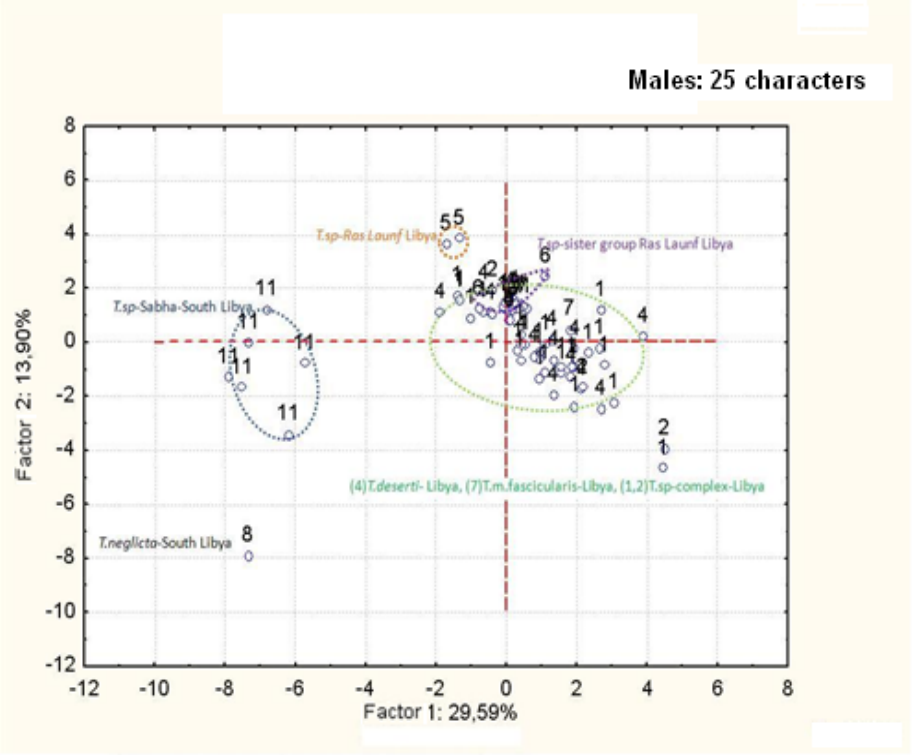


Figure 32. PCA for specimens *T. deserti*-Libya, *T. m. fascicularis*-Libya, *T. sp*-Suirt-Libya, *T. sp*-Sabha-South Libya, *T. mauritanica*-Tripolitania, *T. mauritanica*-Egypt, *T. mauritanica*-Tunisia, *T. mauritanica*-Algeria, and *T. mauritanica*-Morocco. The first and second principal components cover 42.64% of total variance in males, and 39.93%

A. males



B. Females

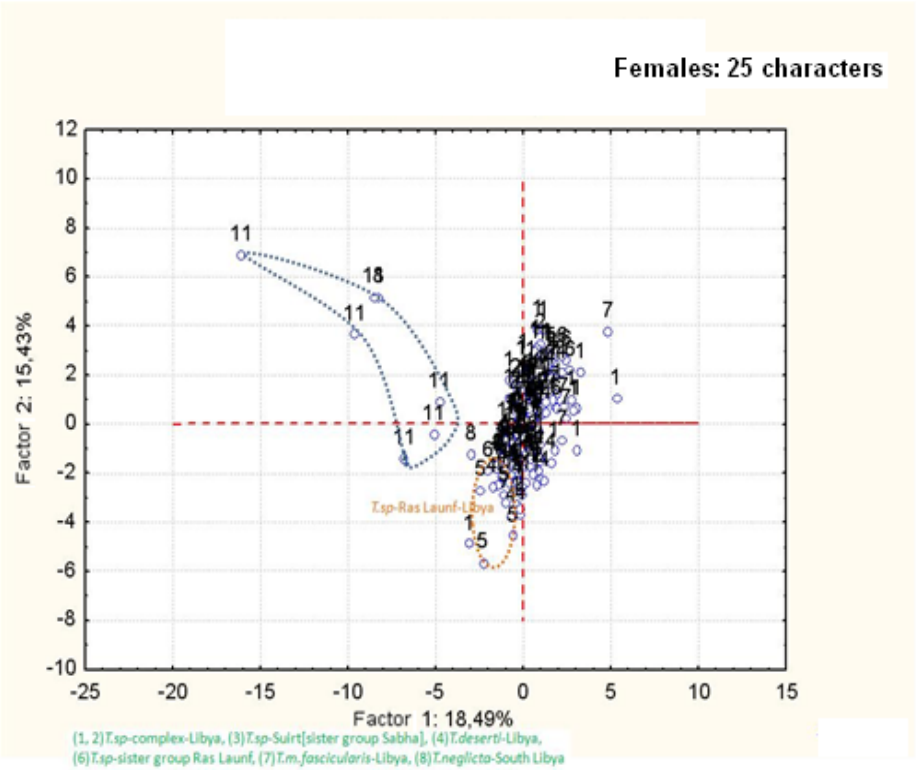


Figure 33. PCA for Libyan specimens, *T. deserti*, *T. m. fascicularis*, *T. sp-complex, T. sp*-Ras Lanuf, *T. sp*-sister group Ras Lanuf, *T. sp*-Suirt, *T. sp*-Sabha, and *T. neglicta*- Gaber-Aown Oasis Lake. The first and second principal components cover 43.49% of total variance in males, and 33.92% in females.

03 MOLECULAR PHYLOGENETIC STUDY

3.1. Introduction

It is very difficult to distinguish between different species and/or subspecies of genus *Tarentola* superficially, many of cryptic species are distinct lineages that are, morphologically, undiagnosable using only external morphological features. The molecular revolution has influenced all areas of biology; molecular data have also revolutionized the study of evolutionary biology and become an important tool for systematic studies, the number of studies using molecular methods in evolutionary biology has greatly increased. The basal techniques of molecular biology are used the same way all over the world, making an exchange of information (methods and results) quick and easy. Today the vast majority of data in phylogenetic reconstruction is biological sequence data (nucleotide or protein); one major advantage of biological sequence data is the increase of phylogenetically relevant information due to the large number of characters that can be obtained by sequencing. Nowadays nucleotide sequences can be efficiently obtained using fast automated sequencing techniques. In the last decades most intraspecific studies using sequence-based genetic markers have focused on mitochondrial DNA, the popularity of mtDNA in these studies can be explained by its maternal inheritance, relatively rapid rate of substitution and relative ease with which it is isolated and analyzed (Avise, 2000). A very important advantage when looking at closely related taxa, especially intraspecific relationships, is that the evolution rate of mtDNA in animals is generally much faster than nuclear DNA. The rates and patterns of mtDNA evolution vary among taxa, and among different regions of mtDNA.

On this background, a phylogenetic study was carried out to investigate the phylogeny of the genus *Tarentola* in North Africa in general and in Libya in particular. Two mitochondrial gene regions and three nuclear gene regions were analyzed. The main objectives of this work are: to generate a phylogeny of the

taxa from Libya and determine their relationships to other major *Tarentola* clades using different molecular markers.

3.2. Material and methods

3.2.1. Material

3.2.1.1. Samples collection

The sample materials examined in this study were collected mainly during two long-term trips in Libya, within the years 2007 and 2008, from 35 localities. In this study 317 tissue specimens representing different local forms of genus *Tarentola* on Libya were used. In addition to the Libyan samples, 76 tissue specimens of different species and subspecies of the genus *Tarentola* from Europe and North Africa were incorporated into the study. These were kindly provided by Ulrich Joger (SHNM-BS- Staatliches Naturhistorisches Museum, Braunschweig, Germany), and Miguel Vences (Technical University Braunschweig, Germany). As a source of DNA, tail muscle, liver tissues, heart tissues or blood tissue were taken immediately after the animals were collected during the field-work, preserved in 100% ethanol, and stored at – 20°C until further experiments. A list of species, general area of sampling and the number of specimens examined in this study are listed in the appendix.

3.2.1.2. Equipment

All analytical instruments used in the present study are listed as following:

Instruments	**Supplier**
ABI GeneAmp PCR System 9700	Applied Biosystems
Agagel Maxi	Biometra
Agagel Standard	Biometra
Authorized Thermal Cycler (PCR) Mastercycler gradient	Eppendorf

Automated sequencer ABI Prism® 3130 Genetic XL	Applied Biosystems
Centrifuge 5415D	Eppendorf
Centrifuge 5424	Eppendorf
Centrifuge 5804	Eppendorf
Centrifuge Minispin 5452	Eppendorf
Certified thin wall 96x0.2 ml	Star Lab
Eigth-Canal pipette	Eppendorf
Electronic Precision Balance U4100	Satorius
Electrophoresis power supply 125	Biometra
Electrophoresis standard power pack p25	Biometra
Gloves rotiprotect Latex	Roth
Gloves rotiprotect Nitril	Roth
Laboratory Parafilm	Roth
Magnetic drive RET	Janke & Kunkel
Microcentrifuge tubes1.5 ml	Star Lab
Micropipettes set (10, 20, 200, and 1000 µl)	Eppendorf
Mini Laboport Diaphragm Vacuum Pump-N86 KN.18	KNF Neuberger
Mixing Block MB-102	Bioer
Multipette Plus	Eppendorf
PCR tubes 0.2 ml	Biozym
PCR tubes with attached flat caps 0.2 ml	Star Lab
QIAquick spin columns	Qiagen
Systems analysis and gel documentation Biovision+ 3000.WL / 26MX	PEQLAB
Thermocycler Primus 25 advanced	Clemens
Thermocycler T1	Biometra
Vortex G-560E	Bohemia
Vortex REAX2000	Heidolph

3.2.1.3. Chemicals

Commonly used chemicals, enzymes and other materials were purchased at standard grade from the following companies:

Chemicals, Enzymes and other Material	Supplier
Acetic acid	Applichem
Agarose Low EED	Applichem
Primers	Operon
BigDye 3.1 chemistry	Applied Biosystems
Ethidium bromide 1%(10 mg/ml)	Roth
ddH_2O	
EDTA	Applichem
Ethanol absolute	Sigma-Aldrich
Gene Ruler 100bp DNA ladder (100-1000bp)	Fermentas
Lambda DNA/EcoRI+HindIII Markers	Promega
Isopropanol	Applichem
NaCl	Applichem
Proteinase K (10 mg/ml)	Roth
Sodium acetate	Applichem
Sodium dodecyl sulfate (SDS)	AppliChem
Tris	Roth
Blue/Orange Loading Dye	Promega
Hi Day	Applied Biosystems
Go Taq ®DNA Polymerase	promega
Taq green buffer	promega

PE (washing buffer)	Qiagen
PB (binding buffer)	Qiagen
TBE	Applichem
dNTP´s	Promega

3.2.1.4. Buffers and solutions

Buffers and solutions for molecular biology work used in this study and their components

Stock Solutions	**Ingredients**
Agarose gel solution	0.50 g 1% Agarose gel, 50 ml TAE buffer, 1µl ethidium bromide
TAE Buffer	Tris-base 242.0 g, Glacial Acetic Acid 57.1 ml, EDTA 37.2 g, pH 8.5, make up on a litter with dH_2O
Extraction buffer	2 ml Tris 1M pH8, 4 ml NaCl 5M, 4 ml EDTA 0.5M pH8, 190 ml ddH_2O steril
Buffer PB (binding buffer)	Guanidine hydrochloride, isopropanol
Buffer PE (washing buffer)	10 mM Tris-HCL pH 7.5, 80% ethanol (Note: add 96-100% ethanol to the buffer before used)

3.2.1.5. Oligonucleotide primers

Primers used to amplify and sequence mitochondrial DNA and nuclear gene regions are listed as following, all primers used in this study were synthesized by eurofins mwg/operon.

Primer Name	Sequences 5`- 3`	Source
12S rRNA gene primers		
12S-AL	5`-AAACTGGGATTAGATACCCCACTAT-3`	Kocher et al (1989)
12S-BH	5`-GAGGGTGACGGGCGGTGTGT-3`	Kocher et al (1989)

16S rRNA gene primers		
16S-AL	5`-CGCCTGTTTATCAAAAACAT-3`	Palumbi (1996)
16S-BH	5`-CCGGTCTGAACTCAGATCACGT-3`	Palumbi (1996)
16SR3	5`-TTTCATCTTTCCCTTGCGGTAC-3`	Hrbek & Larson (1999)
16SL3	5`-AGCAAAGAHYWWACCTCGTACCTTTTGCAT-3`	
C-*mos* gene primers		
G73	5`-GCGGTAAAGCAGGTGAAGAAA-3`	Saint et al (1998)
G74	5`-TGAGCATCCAAAGTCTCCAATC-3`	Saint et al (1998)
CO8	5`-GCTTGGTGTTCAATAGACTGG-3`	Han et al (2004)
CO9	5`-TTTGGGAGCATCCAAAGTCTC-3`	Han et al (2004)
RAG2 gene primers		
EM1-F	5`-TGGAACAGAGTGATYGACTGCAT-3`	Gamble et al (2008a)
EM1-R	5`-ATTTCCCATATCAYTCCCAAACC-3`	Gamble et al (2008a)
PY1-F	5`-CCCTGAGTTTGGATGCTGTACTT-3`	Gamble et al (2008a)
PY1-R	5`-AACTGCCTRTTGTCCCCTGGTAT-3`	Gamble et al (2008a)
Phosducin gene primers		
PHOF2	5`-AGATGAGCATGCAGGAGTATGA-3`	Bauer et al (2007)
PHOR1	5`-TCCACATCCACAGCAAAAAACTCCT-3`	Bauer et al (2007)

3.2.2. Methods

3.2.2.1. DNA extraction

Genomic DNA was isolated from muscle or blood tissue preserved in 95-100% ethanol using a standard salt extraction protocol (modified after Bruford et al. 1992), as following: Small aliquots of sample material were digested by incubation at 55°C for 2-4 hours or overnight at 37°C in 410 µl extraction buffer containing (2 ml Tris 1M pH8, 4 ml NaCl 5M, 4 ml EDTA 0.5M pH8, 190 ml ddH_2O steril), plus 80 µl of 10% SDS and 10-15 µl of proteinase K (10 mg/ml). After the tissues were completely histolysed, centrifuging for 5 minutes at 13000

rpm, transfer of supernatant in a new vessel and adding 180 µl NaCl solution, it was mixed (turn Eppi. ca. 50 times or vortex it 30 seconds) and subsequently centrifuged for 5 minutes at 13000 rpm. Then supernatant was transferred quickly in a new vessel, and 420 µl cooled Isopropanol added (mix it gently), and centrifuged for 5 minutes at 13000 rpm, and supernatant carefully removed and discarded. The extracted DNA was washed with 250 µl 80% ethanol (turn Eppi. ca. 30 times), and supernatant carefully removed and discarded (the previous step repeated twice). Dried (alcohol removed completely by drying for 30 minutes at 37°C in the mixing block), and re-dissolved the pellet was in 100 µl ddH_2O, and kept at room temperature for 1 hour. Then, DNA stock solutions were kept at – 20°C until further experiments or used directly. To determine the approximate concentration and quality of the extracted DNA, 3 µl of each DNA solution were loaded onto a 1% agarose gel containing ethidium bromide. DNA concentration was estimated by comparison of fluorescence intensities to a sample of known DNA content (DNA marker).

3.2.2.2. Amplification of target fragments

In the last decades, PCR has rapidly evolved in the field of molecular biology. PCR is a primer-mediated enzymatic amplification of specifically DNA sequences. The "chain reaction" of the technique refers to an increase in the amount of target DNA obtained through successive cycles of amplification. The basic protocol of PCR is as follows: Double stranded DNA (template) is denatured at high temperature to form single strands, short oligonucleotide primers bind at lower annealing temperature to the single strand complementary templates at the ends flanking the targeted sequence, the temperature is raised for synthesis, by primer extension of the target sequences, the newly synthesized double stranded DNA target sequences are denatured at high temperature, and the cycle is repeated (Wolfe and Liston, 1998). In this study PCR was done in a total volume of 25 µl as follows:

3 µl	template (whole DNA)
5 µl	DNA green buffer
0.1 µl	go Tag DNA polymerase
0.5 µl	10 mM dNTP mix
1 µl	10 µM forward primer
1 µl	10 µM reverse primer
14.4 µl	ddH_2O
25 µl	Total volume

In total 2596 bp were amplified from the samples in this study: Two mitochondrial marker genes, partial12S rRNA (372bp) and two fragments of 16S rRNA (448bp and 604bp respectively), and three nuclear marker genes, the partial *C*-mos (424bp), the partial Recombination-Activating Gene 2 (RAG2, 387bp), and the partial Phosducin (361bp). Polymerase chain reactions with specific primers situated in the flanking regions of the target fragments were preformed to amplify the fragments of interest. PCR reactions were performed in Applied Biosystems, Biometra, Clemens and Eppendorf termocyclers with different temperature profiles, depending on the primers and the target fragment according to the following programs:

PCR conditions for the amplification of 12S rRNA gene and 16S rRNA gene

Cycles	Temperature & Duration	
Cycle 1	94°C 90 sec	
Cycle 2	94°C 30 sec	
	45°C 45 sec	
	72°C 60 sec	2- 35 cycles
Cycle 36	72°C 10 min	
Cycle 37	4°C pause	

PCR conditions for the amplification of C-*mos* gene

Cycles	Temperature & Duration	
Cycle 1	94°C 3 min	
	48°C 45 sec	
	72°C 1 min	
Cycle 2	94°C 45 sec	
	48°C 45 sec	
	72°C 1 min	2-35 cycles
Cycle 36	72°C 6 min	
Cycle 37	4°C pause	

- Source: Saint et al. 1998

PCR conditions for the amplification of Rag 2 gene

Cycles	Temperature & Duration	
Cycle 1	94°C 5 min	
Cycle 2	94°C 30 sec	
	52°C 45 sec	
	72°C 1 min	2-32 cycles
Cycle 33	72°C 5 min	
Cycle 34	4°C pause	

- Source: Gamble et al. 2008

PCR conditions for the amplification of Phosducin gene

Cycles	Temperature & Duration	
Cycle 1	95°C 2 min	
Cycle 2	95°C 35 sec	
	50°C 35 sec	
	72°C 95 sec	2-34 cycles
Cycle 35	4°C pause	

- Source: Greenbaum et al. 2007b

3.2.2.3. Purification

QIAquick PCR Purification Kit Protocol using a microcentrifuge was used to obtain pure DNA, this kit is designed to purify single or double-stranded DNA fragments from PCR or other enzymatic reactions, using QIAquick spin columns in a microcentrifuge. The PCR product was purified as following: 110 µl of PB buffer were added to 22 µl of the PCR product (5 volume of PB buffer to 1 volume of PCR product), a QIAquick spin column was placed in a provided 1.5 ml microcentrifuge tube. To bind DNA, the sample was applied to the QIAquick column and centrifuged for 2 min at 13,200 rpm. Flow-through was discarded; the QIAquick column was placed back in the same tube. To wash, 450 µl of PE buffer were added to the QIAquick column and centrifuged for 2 min at 13,200 rpm. Flow-through was discarded and the QIAquick column was placed back in the same tube, and the column was centrifuged for an additional time 2 min at 13,200 rpm to get clean DNA product. The QIAquick column was placed in a new clean 1.5 ml microcentrifuge tube, 50 µl ddH_2O were added to the center of the QIAquick membrane, the column was left standing for 1 min, and then centrifuged for 1 min at 13,200 rpm to get purified DNA. To be sure the purified products were checked on gel electrophoresis; then the products were stored at -20°C until further experiments.

3.2.2.4. Agarose gel electrophoresis

Agarose gel electrophoresis is a method used in molecular biology to separate DNA strands by size, and to determine the size of the separated strands by comparison to strands of known length. The agarose gel was prepared by dissolving agarose powder in electrophoresis buffer (TAE Buffer) at the desired concentration and heating in a microwave oven until complete melting, after cooling down of the agarose solution to about 60°C, ethidium bromide at a final concentration of 0.5 µg/ml was added to the gel at this point to facilitate visualization of DNA after electrophoresis, and the agarose solution was poured

to the tray (because ethidium bromide is suspected to cause cancer, all steps involving ethidium bromide were carefully performed under the fume hood). After that the solution solidified at room temperature. For electrophoresis a horizontal electrophoresis apparatus Biometra was used. Before loading on the gel, samples were mixed with DNA loading buffer. Electrophoresis was run at a voltage of 80 mV; to estimate the size of nucleic acids, a 1 kb or a 100 bp DNA marker was run parallel to the samples in the same gel. Systems analysis and gel documentation Biovision+ 3000.WL / 26MX was used to analyze the gel photographically under UV-light.

3.2.2.5. Sequencing

The sequencing reactions were carried out on a 3130XL automated sequencer (Applied Biosystems) as following: For the subsequent sequencing reactions 10 µl total volume were used; containing between 2-3 µl of cleaned PCR product, 0.5 µl BigDye 3.1 chemistry and 0.3 µm primer. The reactions were run in a thermocycler under the following temperature profiles: an initial denaturation for 1 minute at 96°C, followed by 25 cycles: 10 seconds at 96°C, 5 seconds annealing step at 50°C and 4 minutes extension at 60°C. After that products were cleaned by adding 1 µl of a solution containing: 1.5 µl sodium acetate and 250 mM EDTA (pH8) and precipitated with a fourfold volume of 95% ethanol during a 45 minute centrifugation step at 1500 g. The dried samples were eluted with 10 µl HiDye before run on the sequencer.

3.2.3. Molecular phylogenetic analyses

3.2.3.1. Data preparation

When studying and comparing genetic sequence data, it is essential to identify which parts of the sequence are homologous (stemming from the same common ancestor), Mutational differences among sequences can take the form of

insertion or deletions of single or multiple nucleotides or nucleotide replacements making identification of homology more difficult (Page & Holmes, 1998). Alignment methods try to find the most likely pattern of homology by finding the least costly (most parsimonious) set of changes in a group of sequences, each position in an alignment represents a character and each character can have four character states (A, T, C, G), insertion and deletion events cannot be distinguished and hence are indicated by gaps in the alignment. There are several automatic methods for creating alignments, in this study the sequences data were aligned using CLUSTAL-W, as implemented in the program package *MEGA* ver. 4 (Tamura et al. 2007), and the program package CodonCode Aligner ver. 2.0.6 (Coden Code Corporation, 1999). This method (CLUSTAL-W) is the most widely used alignment method, it is based on a three step multiple alignment algorithm: 1) All pairs of sequences are aligned separately to calculate a distance matrix giving the divergence of each sequence pair. 2) A guide tree is calculated on the base of the distance matrix. 3) Finally the sequences are progressively aligned according to the branching order in the guide tree (Thompson et al. 1994). In the present study all sequences were compared with closely related taxa and populations, and in 5'- 3' direction. Further in the case of nuclear genes, *C-mos*, Rag2 and Phosducin (protein-encoding genes), all sequences were checked for indels and the unexpected presence of stop codons which might indicate a non-functional pseudogene had been amplified (all protein encoding genes obtained as an open reading frame without unexpected stop codons) using *MEGA* ver. 4 (Tamura et al. 2007), by translating nucleotide data into an amino acid sequence based on the vertebrate genetic code, to ensure that no stop codons were present. Mitochondrial genes (12S rRNA and 16S rRNA) sequences showed a number of indels across the full range of the sequences. In the sequences gaps were removed manually after rechecking the electropherogram in *Mega* or CodonCode Aligner for the individuals and positions in question. As sequencing did not result in the same quality and length of all sequences, for the final alignment, a compromise was made between using the maximal number of readable positions and maximal

number of individuals. Interpretation of the electropherogram peaks were examined and corrected with using IUPAC-symbol for heterozygous sites, for the phylogenetic analyses unresolved sites, coded as ‘‘N’’ in the alignments were allowed.

3.2.3.2. Data analysis

Reconstructing the phylogeny from DNA sequence alignments is unfortunately not as straightforward as one might expect, and it is rarely possible to confirm that one has arrived at the true conclusion. The inferred phylogenetic tree can be or can be not differing from the true phylogenetic tree. There are no uniquely correct methods for inferring phylogenies. To find the optimal phylogenetic tree for a given dataset, various methods of phylogenetic analysis were used. These methods can be grouped first according to whether they use discrete character states or a distance matrix of pairwise dissimilarities, and second according to whether they result in only a single best tree, or consider all theoretically possible trees (Salemi and Vandamme, 2003). The most widely employed methods of phylogenetic inference are: neighbor-joining, maximum parsimony, maximum likelihood and Bayesian approaches. In the current study basic sequence statistics were obtained with the program *MEGA* ver. 4 (Tamura et al. 2007); neighbor-joining (NJ, a distance method), maximum likelihood (ML), and Bayesian Markov Chain Monte Carlo (B/MCMC) tree sampling are employed.

Neighbor-Joining (NJ) method: this method is based on distance among sequences; the algorithm makes a distance matrix for each pair sequence and compares them. The similarity of the two taxa is counted just like relationship between them. The tree is made starting with the pair that shows the lowest distance, joining the taxon which shows the next lowest distance from the previous (nearest neighbor). After each new topology made the algorithm checks up for the shortest branch length; many different parameters can be used in making a distance matrix, or to calculate the substitution type. The most used parameter is uncorrected ‘‘P’’ distance (Tamura et al. 2007).

Maximum likelihood (ML): discrete method using individual nucleotide data to choose the optimal tree, it is more computationally expensive than distance methods. ML selects the tree that makes the observed data the most likely evolutionary outcome, this approach is characterized by accuracy in inferring molecular phylogenies (Page and Holmes, 1998).

Bayesian Inference: trees may also be constructed by a Bayesian inference method. This method is concerned with the posterior probabilities of hypotheses; it is often employed in modern phylogenetic analysis. Random walk model samples possible trees in proportion to their posterior probability and the proportion which fit a particular hypothesis can be used to evaluate its usefulness (Lewis, 2001).

3.2.3.3. Model test

Hierarchical phylogenetic relationships among sampled taxa were estimated using Bayesian and maximum likelihood optimality criteria. Before inferring phylogenies, it is essential to take into account how the base substitutions in the sequence are to be modeled. In real sequences, some changes occur more frequently than others (for instance, transitions and transversion occur at different frequencies). In animal mtDNA, transitions (a purine [A or G] is exchanged to a purine, or a pyramidine [T or C] is exchanged to a pyramidine) occur more likely than transversion (a pyramidine is exchanged to a purine or a purine to a pyramidine). Various models such as the Kimura 2 parameter and HKY85 models can be incorporated into the analysis to take account of these biases (Lewis, 2001). In current study, two programs for inferring evolutionary models were used: **Moldeltest ver. 3.7,** it is a computer program used for the selection of the model of nucleotide substitution that best fits the data. This program chooses among 56 evolution models. And **Mrmodeltest 2.3**, this program chooses among 24 evolution models. Table 16 summarizes the best-fit models of molecular evolution for each gene partition, as determined by Modeltest 3.7 and Mrmodeltest 2.3, and the size of each gene partition used in phylogenetic analyses.

3.2.3.4. The choosing of the outgroup

With the aim to get a more reliable tree, outgroup taxa are used in relation with our ingroup taxa (studied taxa). The outgroup taxa should not appear within the ingroup branches in tree topology. As outgroup, the best is to use taxa which are close but not too close to the ingroup taxa (sister taxa) and the taxa which are considered to be evolutionary older than the taxa examined. In preliminary analysis *Hemidactylus turcicus* from Cyrenaica-Libya were designated as outgroup, afterward *Tarentola delalandii* from Canary Islands was used as outgroup.

Table16. Models of evolution inferred from Mrmodeltest 2.3 and Modeltest 3.7 programs for each partition.

Partition	Mrmodeltest2.3 evolution model	Modeltest3.7 evolution model	Size of the fragment
12srRNA	GTR+ G	GTR+ G	382 bp
16srRNA-1	GTR+ G	GTR+ G	447 bp
16srRNA-2	GTR+ I+ G	GTR+ I+ G	604 bp
mtDNA (12srRNA,16srRNA-1, and 16srRNA-2)	GTR+ I+ G	GTR+ I+ G	1433 bp
C-mos	HKY+I	HKY+I	424 bp
Rag2	HKY+I	HKY+I	387 bp
Phosducin	SYM+I	TrNef+I	361 bp
Nuclear genes (C-mos, Rag2, and Phosducin)	GTR+I	TVM+I	1172 bp

3.3. Results

For phylogeny reconstruction the following partitions were analyzed:

1- Two mitochondrial gene regions individually (382 bp of 12srRNA, and two fragments of 16srRNA 447 bp and 604 bp respectively).

2- The combined mitochondrial genes (1433 bp [12srRNA and 16srRNA]).

3- Three nuclear gene regions individually (424 bp of C-*mos*, 387 bp of Rag2, and 361 bp of Phosducin).

4- The combined nuclear genes (1172 bp of [C-*mos*, Rag2, and Phosducin]).

3.3.1. Preliminary 12srRNA analysis

The preliminary investigation was based on 440 specimens (437 specimens of different species of genus *Tarentola* are ingroup and 2 specimens of *Hemidactylus turcicus* from Cyrenaica-Libya were designated as outgroup) of which 111 specimens were obtained from genbank. Data consisted of a total of 363 aligned nucleotide positions of 12srRNA gene, Out of 363 characters, 243 (66.9%) were variable and 210 (Pi: 57.9%) of these parsimony informative. Neighbor Joining analyses were used to investigate the evolutionary relationships among different species and subspecies of genus *Tarentola*. To provide support for the resulting tree, bootstrap support values were calculated from 500 pseudoreplicates. As a result nine main clades are recovered, and major phylogenetic relationships resolved (Figure 34).

The first group is a clade (H) consisting of 147 specimens of genus *Tarentola* from a wide geographic range; these include 138 *T. sp* samples from Tripolitania (namely from Tajura, El Garbulli, Misratah, El Sawani, El Sahla, Rass El Lifa, Garian, Yafran, Tarhunah, Msalleta, and Itwellia), 2 *T. sp* samples from South Libya and 7 specimens from genbank *T. mauritanica* from East Italian Islands (Lampedusa and Conigli), all together form strongly supported monophyletic group, bootstrap value was 0.93 .

The second group is a clade (G) composed of 11 specimens, 7 samples of *T. sp* from north-central Libya and 4 samples of *T. sp* from south Libyan Sahara (namely from El Shwayrif, Sabha and Germa), this clade supported as monophyletic group with high bootstrap support (0.71).

The third group is a clade (F) containing 65 specimens, one sample of *T. deserti* from Algeria, 4 samples of *T.deserti* from Tunisia and 60 specimens of *T. sp* from Tripolitania-Libya (namely from El Sahla, Rass El Lifa, Misratah, Azzawiyah and Itwellia), this clade was resolved and supported as monophyletic group with high bootstrap value (0.80) .

The fourth group is a clade (E) composed of 13 specimens; 9 samples of *T. sp* from Tunisia and 4 samples of *T. mauritanica* from genbank from East Italian Islands (Lampedusa and Conigli), this relationship was strongly supported as monophyletic group by bootstrap (0.92).

The fifth group is a clade (D) made up of 30 specimens of *T. sp* from north-east Libya (Cyrenaica: namely from Ras Lanuf, Marsa El Prega, Sidi Massod, Taknis, Ajdabiya, Banghazi, Desert road Ajdabiya-Tobruk and Tobruk), this clade was resolved as monophyletic group with high supported bootstrap (0.74).

The sixth group is a clade (C) composed of 31 specimens; 9 samples of *T. m. fascicularis* from Egypt (namely from Sanai) and 22 specimens of *T. sp* from Cyrenaica (namely from Sidi Massod, Um Arrizam, Desert road Ajdabiya-Tobruk and Tobruk), this clade was resolved as monophyletic group, although statistically weakly supported (bootstrap value 0.57).

The seventh group is a clade (B) containing 5 samples; one specimen of *T. neglecta* from Algeria and 2 samples identified morphologically as *T. neglecta* from southern Libyan Oases (Gaber Aown Oasis Lake and Mandria oasis), and a sister taxa made up of 2 *T. mindiae* from Egypt, these relation is highly supported by bootstrap (0.79) .

The eighth group is a clade (A) composed of 53 specimens (of which 33 specimens obtained from Genbank); 45 *T. mauritanica* from Europe and Morocco, one specimen of *T. deserti* from Morocco, one specimen of *T. boehmei* from Morocco, and 6 specimens of *T. angustimentalis* from Canary Islands, this clade was weakly supported by bootstrap.

The ninth group is contains 77 specimens (72 specimens obtained from Genbank) and can be divided into several subclades of Makariogecko (*T. boettgeri, T. delalandii, T. gomerensis, T. darwini, T. rudis, T. caboverdianus, T. gigas*), these relationship is strongly supported by bootstrap (0.76).

Clade composed from one specimen of *T. americana* from Guantanamo (Cuba).

One subclade consisting of two specimens of *T. ephippiata* from Senegal, form a monophyletic sister lineage to three specimens of *T. annularis* from Egypt, this relationship was weakly supported by bootstrap.

According to this result (12srRNA), the preliminary OTUs were defined (for morphological study).

In order to conduct further analyses, all identical haplotypes were collapsed (we reduced the number of specimens in each group /or clade to a limited number), resulting in small number of haplotypes being analysed.

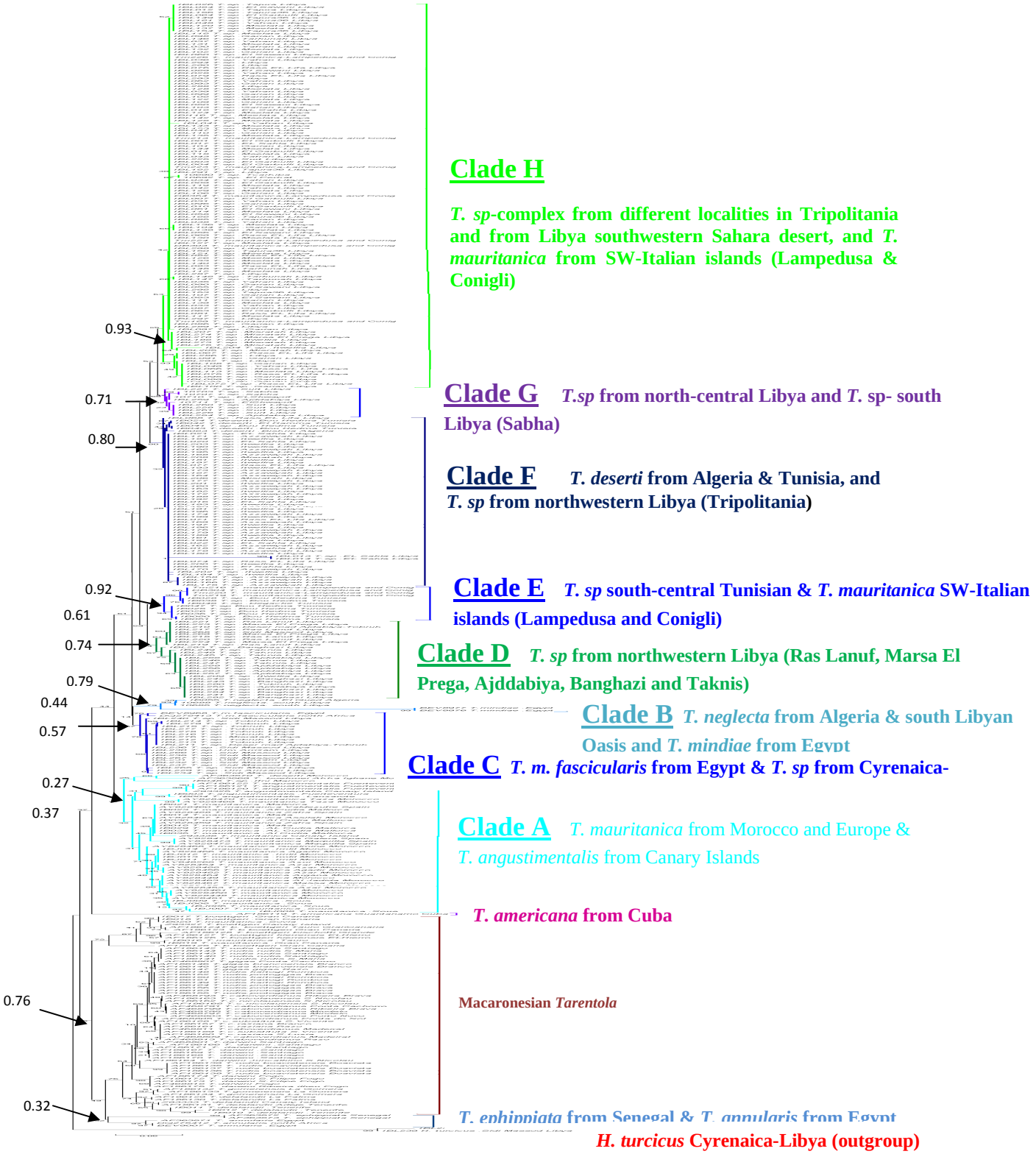


Figure 34. Neighbor-Joining phylogenetic tree, based on partial 12srRNA sequence 363 bp of 440 specimens, depicting the relationships among holotypes, and with *Hemidactylus turcicus* designated as outgroup. Values near the branches correspond to bootstraps values based on 500 pseudoreplicates

3.3.2. Phylogeny based on 12srRNA analysis

This study includes 68 specimens of genus *Tarentola* (11 obtained from genbank), of which 67 are ingroup, and one specimens of *T. delalandii* was designated as outgroup. Data consisted of a total of 382 aligned nucleotide positions of 12srRNA, the average of nucleotide frequencies was: f (A) = 0.32, f (C) = 0.32, f (G) = 0.19, f (T) = 0.17. Out of 382 characters, 150 (39.3%) were variable and 130 (Pi: 34%) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the result of the three methods of analysis were largely congruent and supported the same tree topology. General-time-reversible model with a gamma model of among site rate variation (GTR+G) of molecular evolution were chosen. Calculation of the likelihood scores and choice of the best model of sequence evolution was carried out using Modeltest ver. 3.7 and Mrmodeltest ver. 2.3, under the Akaike Information Criterion.

A Bayesian analysis was performed using Mr.Bayes ver.3.1 (Huelsenbeck et al, 2005). The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 1×10^{6} generations, and saving tree in each 100^{th} generation using a GTR+G model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (2500 samples) from the burnin were discarded. The remaining trees were combined, and a 50% majority-rule consensus tree was generated (Figure 35).

The maximum likelihood (ML) analyses were performed using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics platform, CNRS – Université Montpellier II. The best-fit model (GTR+G) determined by Modeltest ver. 3.7, maximum likelihood searches were performed

with a heuristic search. We used the GTR model of evolution as implemented in PhyML program. To provide support for the resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping.

The Bayesian tree can be divided into nine distinct and well-supported evolutionary lineages. Major phylogenetic relationships resolved, the monophyly of *T. boettgeri* of Gran Canaria; *T. angustimentalis* of Canary islands, *T. mauritanica* of Canary Islands, Malta, Morocco; *T. mindiae* of Egypt, *T. neglecta* of South Libya Oases and Algeria; *T. m. fascicularis* of Egypt, *T. sp* of Um Arrizam and Sidi Massod (Green mountain); *T. sp* of Ras Lanuf, Marsa El Prega, and Taknis; *T. sp* of Tunisia, *T. mauritanica* of Lampedusa and Conigli islands (Italy); *T. deserti* of Tunisia, *T. sp* of Azzawiyah, El Sahla, Rass Lifa and Itwellia (Libya); *T. sp* of Sabha, El Shwayrif, Suirt; and *T. sp* of Tripolitania, and Tcarkiba, *T. mauritanica* of East Italian Islands were clearly recovered. The congruent tree topology was identified by Maximum likelihood analyses (Figure 36).

1- Group composed of five specimens of European and Moroccan *T. mauritanica,* and two specimens of *T. angustimentalis* from Canary Islands (Clade A); *T. mauritanica* from Malta, Mallorca and Morocco was resolved paraphyletic with respect to *T. angustimentalis*, however this relationship was weakly supported.

2- Group consisting of specimens from a broad geographic range (clade B), *T. mindiae* from Egypt, *T. neglecta* from Algeria, and two specimens identified morphologically as *T. neglecta* from southern Libyan Oases (Gaber Aown Oasis Lake and Mandria Oasis). Specimens of *T. neglecta* from south Libyan oases and Algerian form a strongly supported monophyletic group by both bootstrap and Bayesian posterior probability, 0.99 and 1.00 respectively; *T. mindiae* form a monophyletic sister lineage to *T. neglecta* group with strong support by both bootstrap and Bayesian posterior probability, 1.00 and 1.00 respectively.

3- A clade including *T. sp* from Cyrenaica (Al Jabal Al Akhdar) and *T. m. fascicularis* from Egypt, this clade is strongly supported as a group (clade C).

4- A clade from north-east Libya (Cyrenaica), composed of specimens of *T. sp* from Taknis, Marsa El Prega and Ras Lanuf (clade D), this clade is weakly supported by bootstrap 0.59, but showed high Bayesian posterior probability support 0.96; this clade can be divided into subclades. One includes the specimens from Ras Lanuf and Marsa El Prega, all are identical for these regions of the 12SrRNA, and sister taxa to these are specimens from Taknis, this relation is well supported by both bootstrap and Bayesian posterior probability (0.98 and 1.00 respectively), they differ from the Ras Lanuf and Marsa El Prega samples by just 9 nucleotide substitutions.

5- Clade E, a lineage made up of specimens of *T. sp* from Tunisia and *T. mauritanica* from south-west Italian islands (Lampedusa and Conigli), this clade is weakly supported by bootstrap (0.59), but strongly supported by Bayesian posterior probability (0.96), and can be divided into subclades. The first one consists of specimens of *T. mauritanica* from south-west Italian Islands; all are identical for these regions of 12srRNA. The second is its sister group, and consists of the samples of *T. sp* from Tunisia, this relationship is well supported by both bootstrap and Bayesian posterior probability, 0.89 and 1.00 respectively. They differ just by 3 nucleotide substitutions.

6- Clade F, this clade is very strong supported by Bayesian posterior probability (0.99), but moderate supported by bootstrap (0.65). This lineage includes one specimen of *T. deserti* from Tunisia and six specimens of *T. sp* from north-west Tripolitania (namely Azzawiyah, El Sahla, Rass El Lifa, and Itwellia). The specimens from El Sahla, Rass El Lifa and Itwellia are identical in these regions of 12rRNA with the sample

from Tunisia; the samples from Azzawiyah differ by just 2 nucleotide substitutions from the remaining samples in this group.

7- Clade G, includes the samples of *T. sp* from north-central Libya (Suirt), Ajddabiya, and south Libyan Sahara desert (Sabha and El Shwayrif). This clade is strongly supported by both bootstrap and Bayesian posterior probability, 0.79 and 1.00 respectively. The clade can be divided into subclades. One includes the samples of Suirt and Ajddabiya, and second subclade consists of Sabha and El Shwayrif samples; the two subclades differ by 14 nucleotide substitutions.

8- Clade H, this clade is composed of samples from a wide geographic range. This clade is moderately supported by bootstrap (0.62), but well supported by Bayesian posterior probability (0.97). This clade can be divided into subclades: The first one includes *T. sp* samples from Tcarkiba and El Perkat in south Libya, and from Tripolitania (Itwellia, Tajura, Misratah, Tarhunah, and Msalleta). Sister taxa to these is south-west Italian islands (Lampedusa and Conigli) samples of *T. mauritanica,* these are all identical for these regions of 12srRNA. This relationship is well supported by both bootstrap and Bayesian posterior probability (0.66 and 0.90 respectively). Libyan samples in the first subclade differ from Italian samples by 10 nucleotide substitutions. The third subclade consists of Rass El Lifa and Garian (West Mountain) samples; this group is differing from Italian samples by 8 nucleotide substitutions.

9- On the basis of the tree, one specimens *T. annularis* from Egypt and three specimens *T. boettgeri* from Canary Islands, *T. annularis* is well supported by both bootstrap and Bayesian posterior probability as forming a basal group outside this group (0.80 and 0.95 respectively); specimens of *T. boettgeri* are strongly supported as a monophyletic group by both bootstrap and Bayesian posterior probability (0.99 and 1.00 respectively).

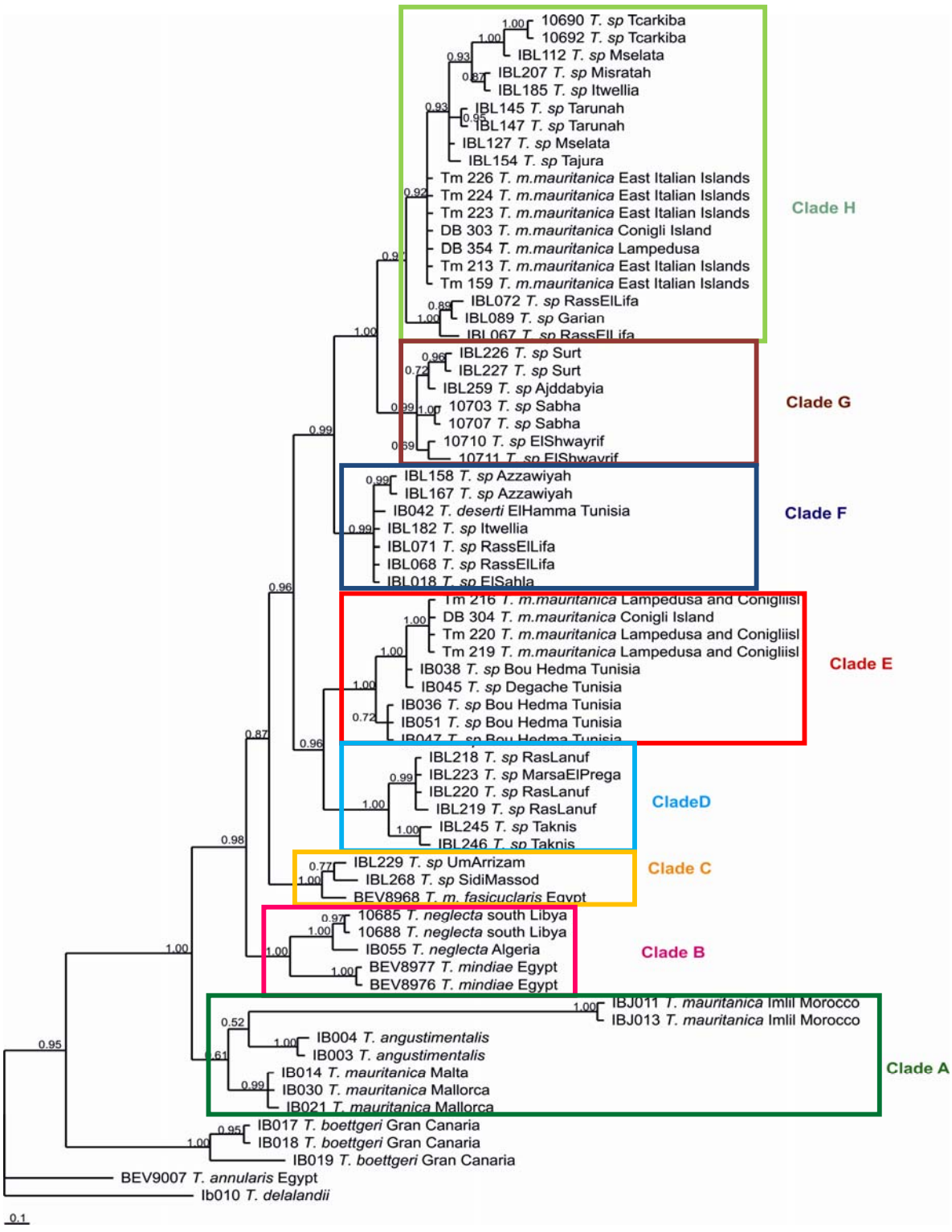


Figure 35. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on partial 12srRNA sequence 382 bp, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.

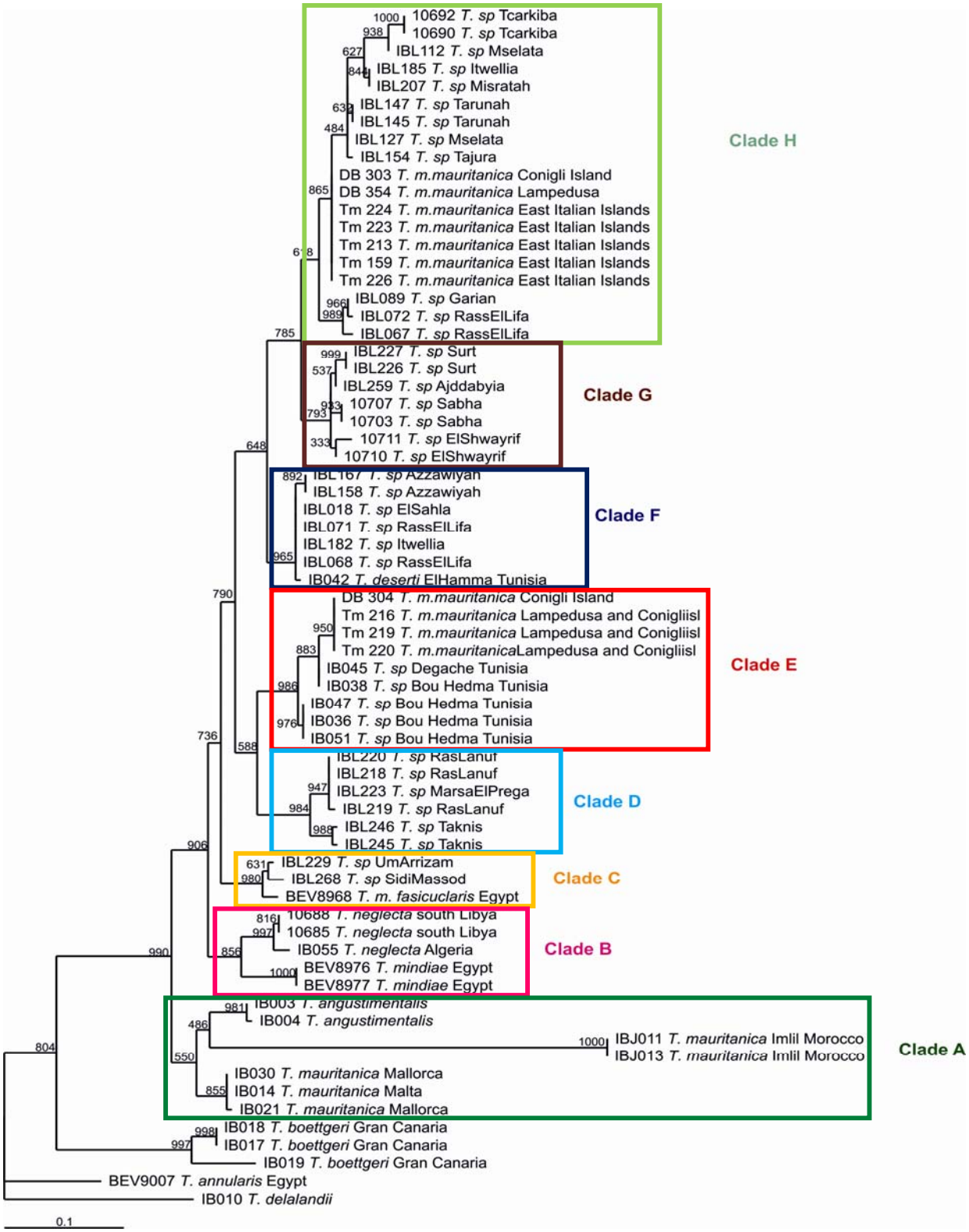


Figure 36. Tree derived from ML analysis using the model explained in the text, based on partial 12srRNA sequence 382 bp. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.

3.3.3. Phylogeny based on 16srRNA sequence data

Two fragments of 16srRNA were studied; the first consisted of a total of 447 aligned nucleotide positions, and the second consisted of a total of 604 aligned nucleotide positions.

3.3.3.1. The first fragment (16srRNA-1)

This study includes 54 specimens of genus *Tarentola*, of which 52 are ingroup, and two specimens of *T. delalandii* were designated as outgroup. Data consisted of a total of 447 aligned nucleotide positions of 16srRNA, the average of nucleotide frequencies was: f (A) = 0.32, f (C) = 0.30, f (G) = 0.18, f (T) = 0.20. Out of 447 characters, 119 (26.6%) were variable and 106 (Pi: 23.7%) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the result of three methods of analysis were largely congruent and supported the same tree topology. General-time-reversible model with a gamma model of among site rate variation (GTR+G) of molecular evolution were chosen. Calculation of the likelihood scores and choice of the best model of sequence evolution was carried out using Modeltest ver. 3.7 and Mrmodeltest ver. 2.3, under the Akaike Information Criterion.

A Bayesian analysis was carried out using Mr.Bayes Ver.3.1. The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 1.5×10^{6} generations, and saving tree in each 100^{th} generation using a GTR+G model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (3750 samples) from the burnin were discarded. The remaining trees were combined, and a 50% majority consensus tree was generated (Figure 37). The congruent tree topology was identified by Maximum likelihood analyses (Figure 38).

The maximum likelihood (ML) analyses were performed using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics platform, CNRS – Universit Université Montpellier II. The best-fit model (GTR+G) was determined by Modeltest ver. 3.7, maximum likelihood searches were performed with a heuristic search. To provide support for resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping.

The nine major clades related to the foremost 12srRNA evolutionary lineages are recovered.

1- Clade A: *T. mauritanica* Malta and Mallorca, *T. angustimentalis* from Canary Islands, all *T. mauritanica* specimens are identical in these regions of 16srRNA, with strong support; *T. angustimentalis* from Canary Islands form monophyletic sister lineage to *T. mauritanica* from Malta and Mallorca, these relation is strongly supported by bootstrap and Bayesian posterior probability, 1.00 and 1.00 respectively.

2- Clade B containing specimens of *T. mindiae* from Egypt, *T. neglecta* from Algeria and two samples identified as *T.neglecta* from South Libyan desert oases. Libyan samples *T.neglecta* formed a sister relationship to *T. neglecta* from Algeria, they differ by 8 nucleotide substitutions, these relation is strongly supported by both bootstrap and Bayesian posterior probability, 0.96 and 1.00 respectively. *T. mindiae* form a monophyletic sister lineage to *T. neglecta* group, this relationship was weakly supported by bootstrap 0.61, but strongly supported by Bayesian posterior probability 1.00.

3- Clade C one specimen of *T. m. fascicularis* from Egypt was placed in a clade together with *T. sp* from Cyrenaica. *T. m. fascicularis* from Egypt formed a sister relationship to *T.sp* from Cyrenaica, they differ by 3 nucleotide substitutions, this relation is also strongly supported by both bootstrap and Bayesian posterior probability, 1.00 and 1.00 respectively.

4- Clade D containing specimens of *T. sp* from Ras Lanuf, Marsa El Prega, Ajdabiya and Taknis. Specimens of *T. sp* from Ras Lanuf and Marsa El Prega are forming a monophylum, all these specimens are identical in these regions of 16srRNA. Sister group to these are *T. sp* from Ajdabiya and Taknis. This relationship is well supported by both bootstrap and Bayesian posterior probability, 0.98 and 1.00 respectively; they differ by 7 nucleotide substitutions.

5- Clade E consists of specimens of *T. sp* from Tunisia, this clade was resolved and supported as monophyletic group with bootstrap and Bayesian posterior probability, 0.76 and 0.94 respectively.

6- Clade F containing specimens of *T. sp* from north-west Tripolitania, this clade supported as monophyletic group with high bootstrap and Bayesian posterior probability, 0.89 and 1.00 respectively.

7- Clade G composed of north-central Libya and south Libyan Sahara samples. This clade is well supported, and consists of two subclades. *T. sp* south Libyan (namely Sabha and El Shwarif), all these specimens are identical in these regions of 16srRNA, *T. sp* from Suirt (north-central Libya) form a monophyletic sister lineage to south Libyan *T. sp,* these relationship is well supported by both bootstrap and Bayesian posterior probability, 0.79 and 0.99 respectively.

8- Clade H containing samples from a wide geographic range, this clade is well supported as a group, and can be divided into subclades. The first, consists of samples of *T. sp* from Western Mountain (Garian and Rass El Lifa). The second, *T. sp* from Tajura, Tarhunah, Msalleta and Misratah formed a sister relationship with the first group; this relationship is well supported by both bootstrap and Bayesian posterior probability, 0.73 and 1.00 respectively. Another subclade containing two specimens of *T. sp* from South Libyan (Tcarkiba and El Perkat in the extreme south-west Libya), these are all identical for these regions of 12srRNA, and differ from

the first subclade by 4 nucleotide substitutions, and from the second subclade by 7 nucleotide substitutions.

9- On the basis of the tree one specimen of *T. a. annularis* from Egypt and three specimens of *T. boettgeri* from Gran Canaria are placed. The monophyly of the *T. boettgeri* was highly supported by both bootstrap and Bayesian posterior probability, 1.00 and 1.00 respectively. *T. a. annularis* from Egypt is forming a sister relationship *with T. boettgeri*, but this relationship is weakly supported by both bootstrap and Bayesian posterior, 0.38 and 0.54 respectively.

3.3.3.2. The second fragment (16srRNA-2)

This study was conducted of 55 specimens of genus *Tarentola*, 53 were ingroup and two specimens *T. delalandii* were designated as outgroup. The data consisted of a total of 604 aligned nucleotide positions of 16srRNA, the average of nucleotides frequencies was: f (A) = 0.37, f (C) = 0.30, f (G) = 0.16, f (T) = 0.17. Out of 604 characters, 248 (48.1%) were variable and 224 (Pi: 37.1) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the results were largely congruent and supported the same tree topology. GTR+I+G model of molecular evolution was chosen. Calculation of the likelihood scores and choice of the best model of sequence evolution was carried out using Modeltest ver. 3.7 and Mrmodeltest ver. 2.3, under the Akaike Information Criterion.

A Bayesian analysis was carried out using Mr.Bayes Ver.3.1. The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 1×10^{6} generations, and saving tree in each 100^{th} generation using a GTR+I+G model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (2500 samples)

from the burnin were discarded. The remaining trees were combined, and a 50% majority consensus tree was generated (Figure 39). The congruent tree topology was identified by Maximum likelihood analyses (Figure 40).

The maximum likelihood (ML) analyses were performed using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics platform, CNRS – Université Montpellier II. The best-fit model (GTR+I+G) was determined by Modeltest ver. 3.7, maximum likelihood searches were performed with a heuristic search. To provide support for resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping.

The trees (ML tree and Bayesian tree) were largely congruent, and can be divided into nine distinct evolutionary lineages, with different degrees of statistical supported (bootstrap and Bayesian posterior probability). They were largely congruent with 16srRNA-1 trees (ML and Bayesian trees), they differing in the degrees of statistical support (bootstrap and Bayesian posterior probability), and arrangement of clades positions.

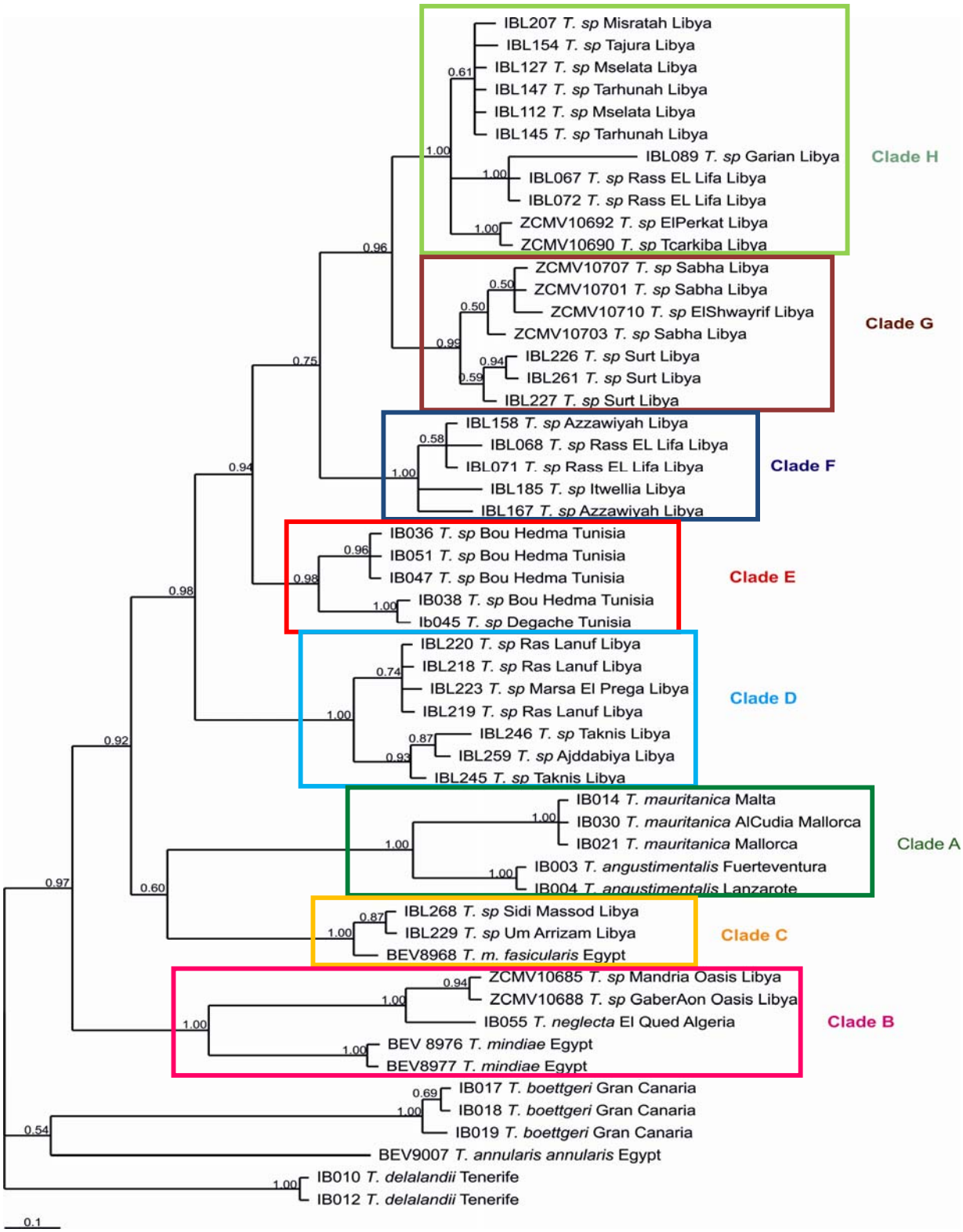


Figure 37. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on partial 16srRNA-1 sequence 447 bp, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.

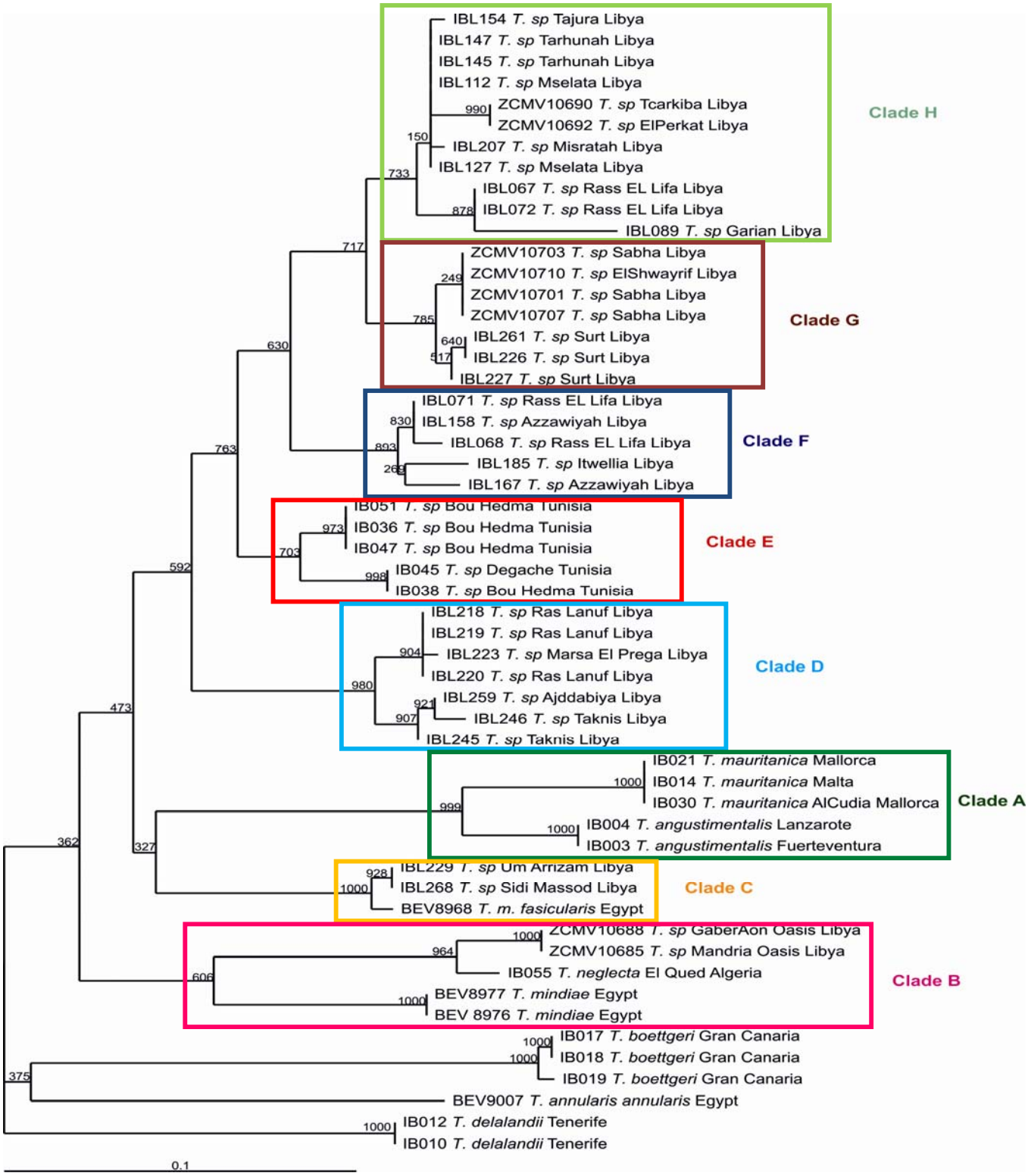


Figure 38. Tree derived from ML analysis using the model explained in the text, based on partial 16srRNA-1 sequence 447 bp. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.

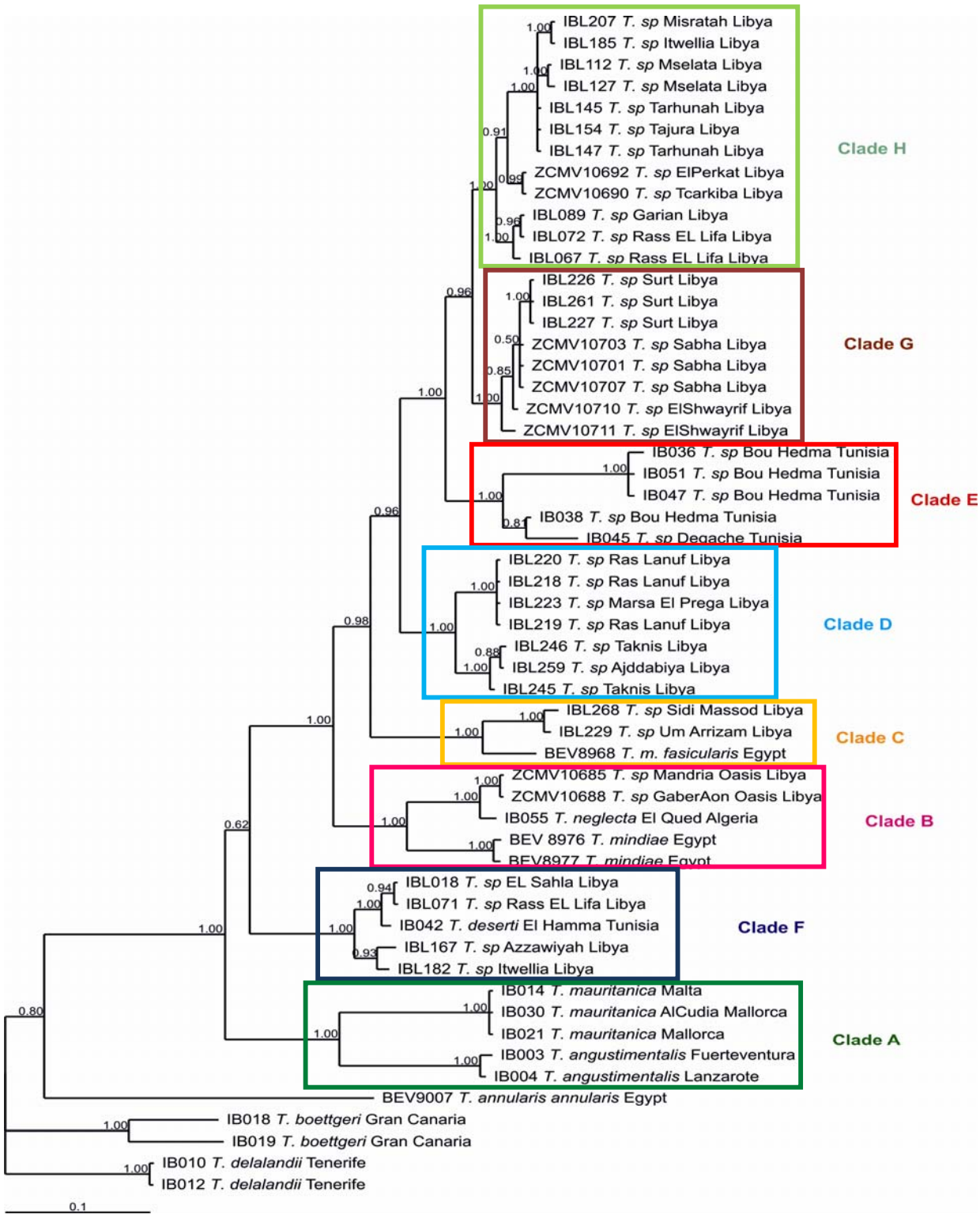


Figure 39. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on partial 16srRNA-2 sequence 604 bp, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.

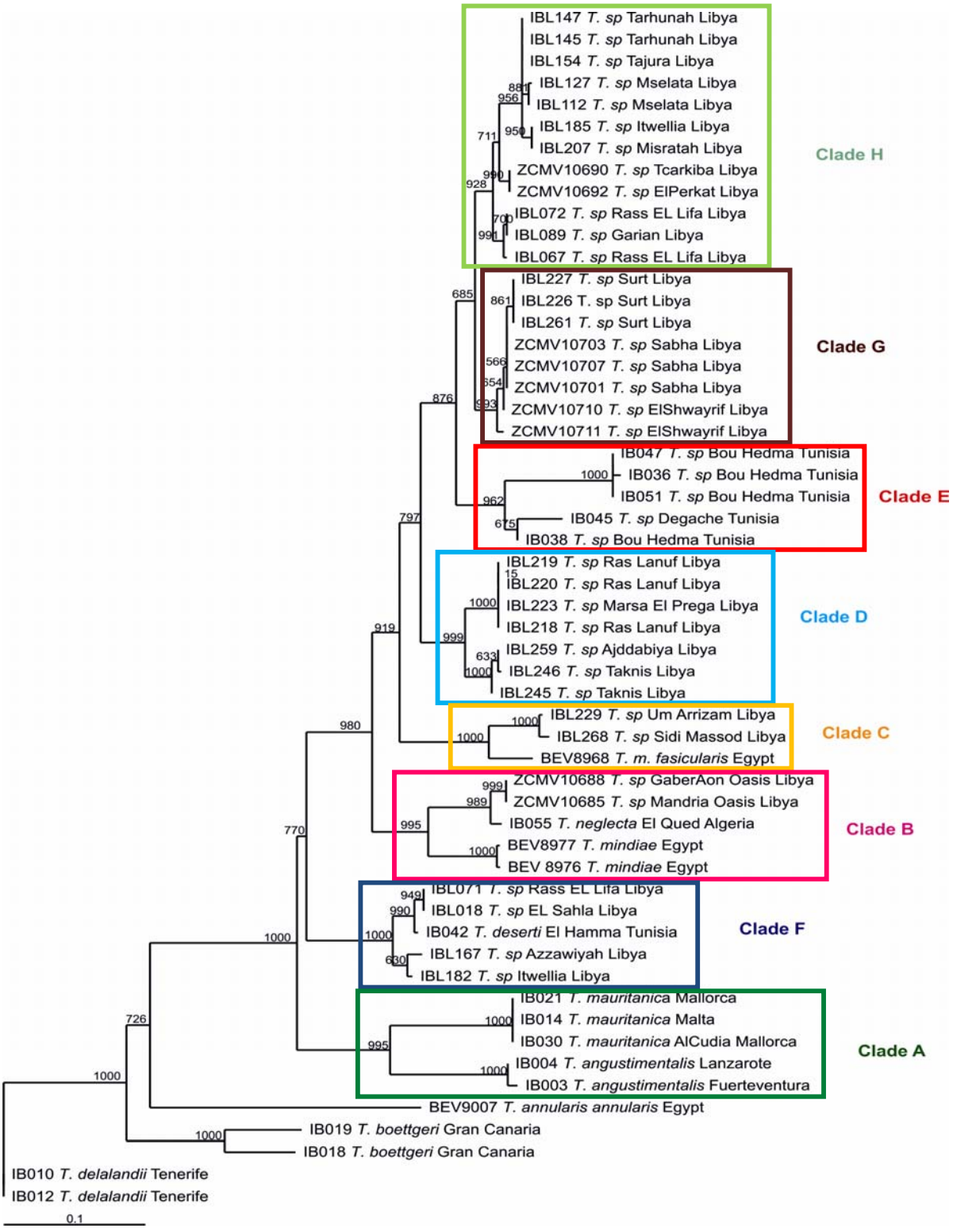


Figure 40. Tree derived from ML analysis using the model explained in the text, based on partial 16srRNA-2 sequence 604 bp. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.

3.3.4. Phylogeny based on combined mtDNA sequence data

Independent analysis of three-gene fragments (12srRNA, 16srRNA-1 and 16srRNA-2) showed that there is no conflict among partitions, and therefore the genes could be analyzed in combination. So the study includes 48 specimens of genus *Tarentola*, of which 47 are ingroup, and one specimen of *T. delalandii* was designated as outgroup. Data consisted of a total of 1433 aligned nucleotide positions of mtDNA, composed of 382 bp 12srRNA, and two fragments of 16srRNA 447 bp and 604 bp respectively. The average of nucleotides frequencies was: f (A) = 0.34, f (C) = 0.31, f (G) = 0.17, f (T) = 0.18. Out of 1433 characters, 493 (34.4%) were variable and 416 (Pi: 29%) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the result of these three analysis methods were largely congruent and supported the same tree topology. GTR+I+G model of molecular evolution was chosen. Calculation of the likelihood scores and choice of the best model of sequence evolution was carried out using Modeltest ver. 3.7 and Mrmodeltest ver. 2.3, under the Akaike Information Criterion.

A Bayesian analysis was carried out using Mr.Bayes Ver.3.1. The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 1×10^{6} generations, and saving tree in each 100^{th} generation using a GTR+I+G model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (2500 samples) from the burnin were discarded. The remaining trees were combined, and a 50% majority consensus tree was generated (Figure 41).

The maximum likelihood (ML) analyses were performed using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics platform, CNRS – Université Montpellier II. The best-fit model (GTR+I+G) was determined by Modeltest ver. 3.7, maximum likelihood searches were performed

with a heuristic search. To provide support for the resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping (Figure 42).

The trees (NJ tree, ML tree and Bayesian tree) were largely congruent. Nine major clades relevant to the major distinct evolutionary mtDNA lineages are recovered, with different degrees of statistical supported (bootstrap and Bayesian posterior probability). The trees were largely congruent with 12srRNA trees, 16srRNA-1 trees and 16srRNA-2 trees, only differing in the degrees of statistical support (bootstrap and Bayesian posterior probability) and arrangement of clades positions.

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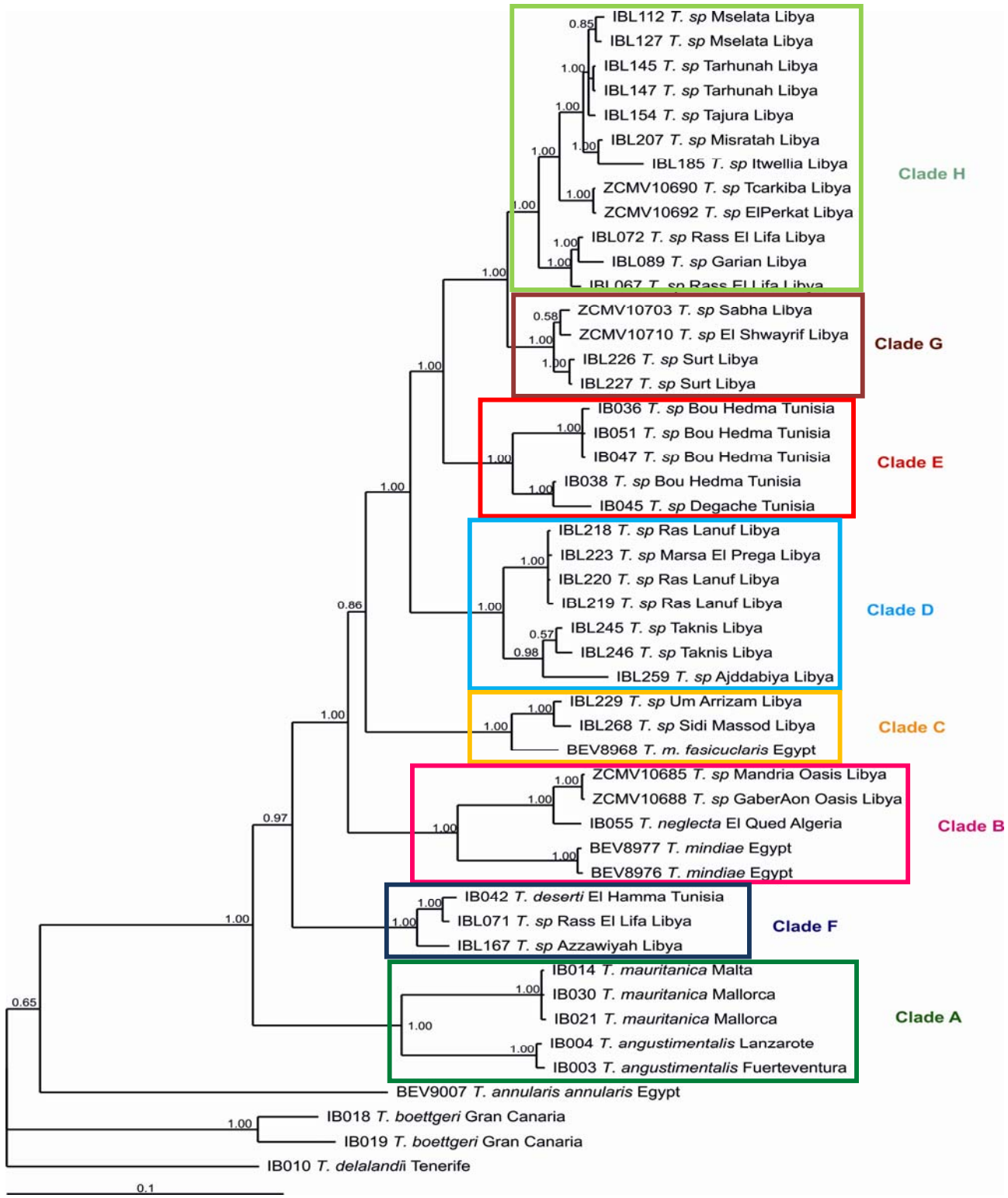


Figure 41. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on 1433 bp mtDNA sequences, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.

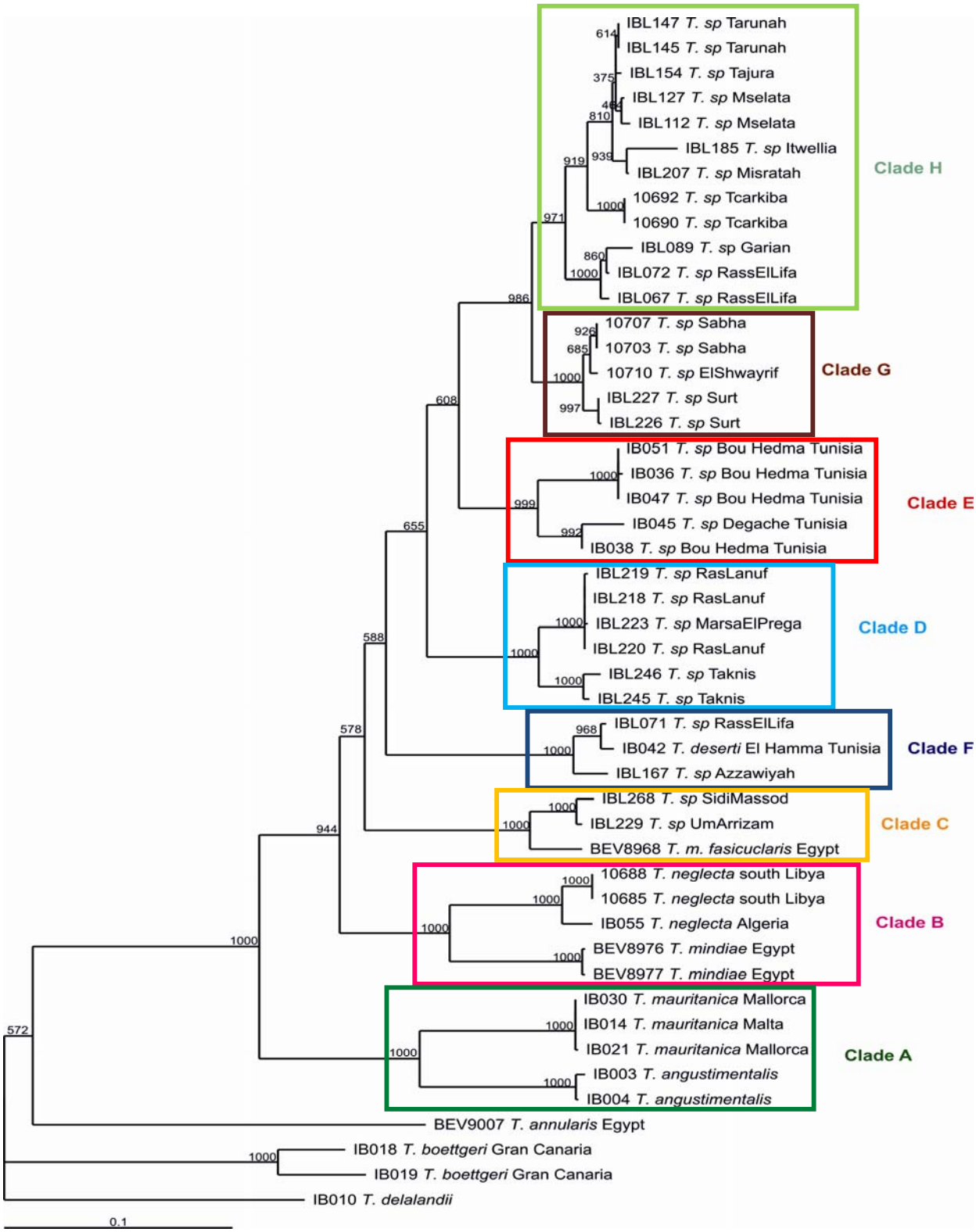


Figure 42. Tree derived from ML analysis using the model explained in the text, based on partial mtDNA sequence 1433 bp. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.

3.3.5. Phylogeny based on C-*mos* nuclear gene sequence data

Our analyses is based on 59 specimens of genus *Tarentola*, of which 57 are ingroup, and two specimens of *T. delalandii* were designated as outgroup. Data consisted of a total of 424 aligned nucleotide positions of *C-mos*. The average of nucleotide frequencies was: f (A) = 0.31, f (C) = 0.21, f (G) = 0.22, f (T) = 0.27. Out of 424 characters, 20 (4.7%) were variable and 8 (Pi: 1.9%) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the result of these three analysis methods were largely congruent and supported the same tree topology. HKY+I model of molecular evolution was chosen. Calculation of the likelihood scores and choice of the best model of sequence evolution was carried out using Modeltest ver. 3.7 and Mrmodeltest ver. 2.3, under the Akaike Information Criterion.

Neighbor Joining analysis was carried out using MEGA ver.4.1. For calculating of gaps/ or missing data positions, pairwise deletion option was selected. Jukes-cantor model of molecular evolution as implemented in MEGA program was chosen. To provide support for the resulting tree, bootstrap support values were calculated from 1000 replicates (Figure 43).

A Bayesian analysis was carried out using Mr.Bayes Ver.3.1. The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 10×10^{6} generations, and saving tree in each 1000^{th} generation using a HKY+I model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (2500 samples) from the burnin were discarded. The remaining trees were combined, and a 50% majority consensus tree was generated (see appendix 3).

The maximum likelihood (ML) analyses were carried out using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics

platform, CNRS – Université Montpellier II. The best-fit model (HKY+I) was determined by Modeltest ver. 3.7, we used HKY85 model of evolution as implemented in PhyML program, and maximum likelihood searches were performed with a heuristic search. To provide support for the resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping (see appendix 4).

The trees were largely uninformative, included an unresolved and lower supported trees topology. Confirming that members of these genera are more closely related to each other, the only exception of synapomorphy links *T. neglecta* from Algeria and South Libya oases with *T. mindiae* from Egypt in one group. This is in accordance with our phylogeny estimated from mtDNA sequences.

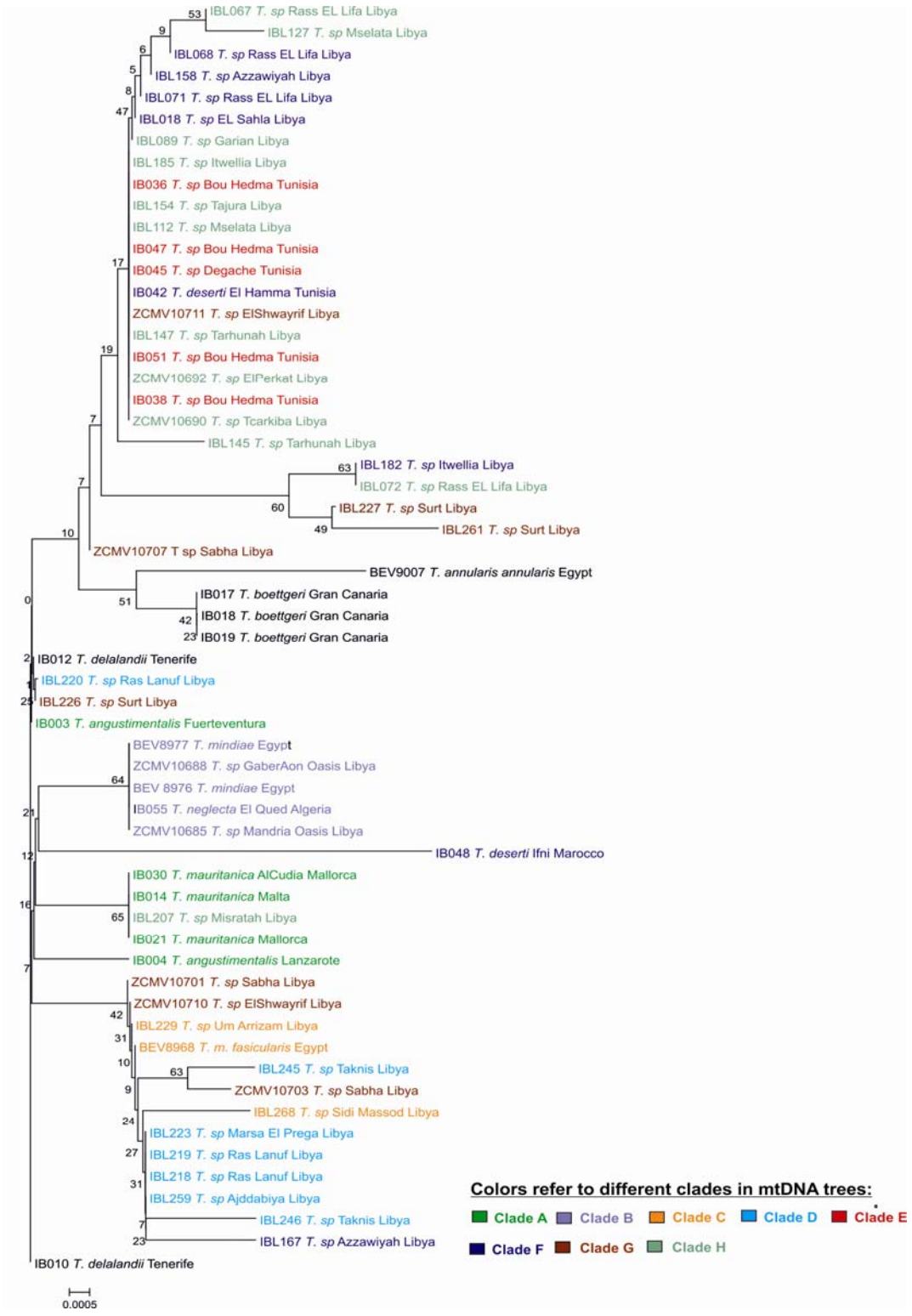


Figure 43. Neighber-Joining phylogenetic tree based on 424 bp C-*mos* sequence; depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup. Values near the branches correspond to bootstraps values based on 1000 pseudoreplicates.

3.3.6. Phylogeny based on Phosducin nuclear gene sequence data

The study includes 59 specimens of genus *Tarentola*, of which 57 are ingroup, and two specimens of *T. delalandii* were designated as outgroup. Data consisted of total of 361 aligned nucleotide positions of Phosducin. The average of nucleotide frequencies was: f (A) = 0.26, f (C) = 0.22, f (G) = 0.25, f (T) = 0.27. Out of 361 characters, 20 (5.5%) were variable and 12 (Pi: 3.3) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the results were largely congruent and supported the same tree topology. TrNef+1 and SYM+1 models of molecular evolution were chosen by Modeltest ver. 3.7 and Mrmodeltest ver. 2.3 respectively, under the Akaike Information Criterion.

Neighbor Joining analysis was carried out using MEGA ver.4.1. For calculating of gaps/ or missing data positions, pairwise deletion option was selected. Jukes-cantor model of molecular evolution as implemented in MEGA program was chosen. To provide support for the resulting tree, bootstrap support values were calculated from 1000 replicates (Figure 44).

A Bayesian analysis was performed using Mr.Bayes Ver.3.1. The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 1.5×10^{6} generations, and saving tree in each 100^{th} generation using a SYM+I model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (3750 samples) from the burnin were discarded. The remaining trees were combined, and a 50% majority consensus tree was generated (see appendix 5).

The maximum likelihood (ML) analyses were carried out using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics

platform, CNRS – Université Montpellier II. The best-fit model (TrNef+I) was determined by Modeltest ver. 3.7, we used TN93 model of evolution as implemented in PhyML program, and maximum likelihood searches were performed with a heuristic search. To provide support for the resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping (see appendix 6).

Our analyses of 361 aligned nucleotide positions of Phosducin yielded uninformative trees including unresolved and moderately statistical supported trees topology.

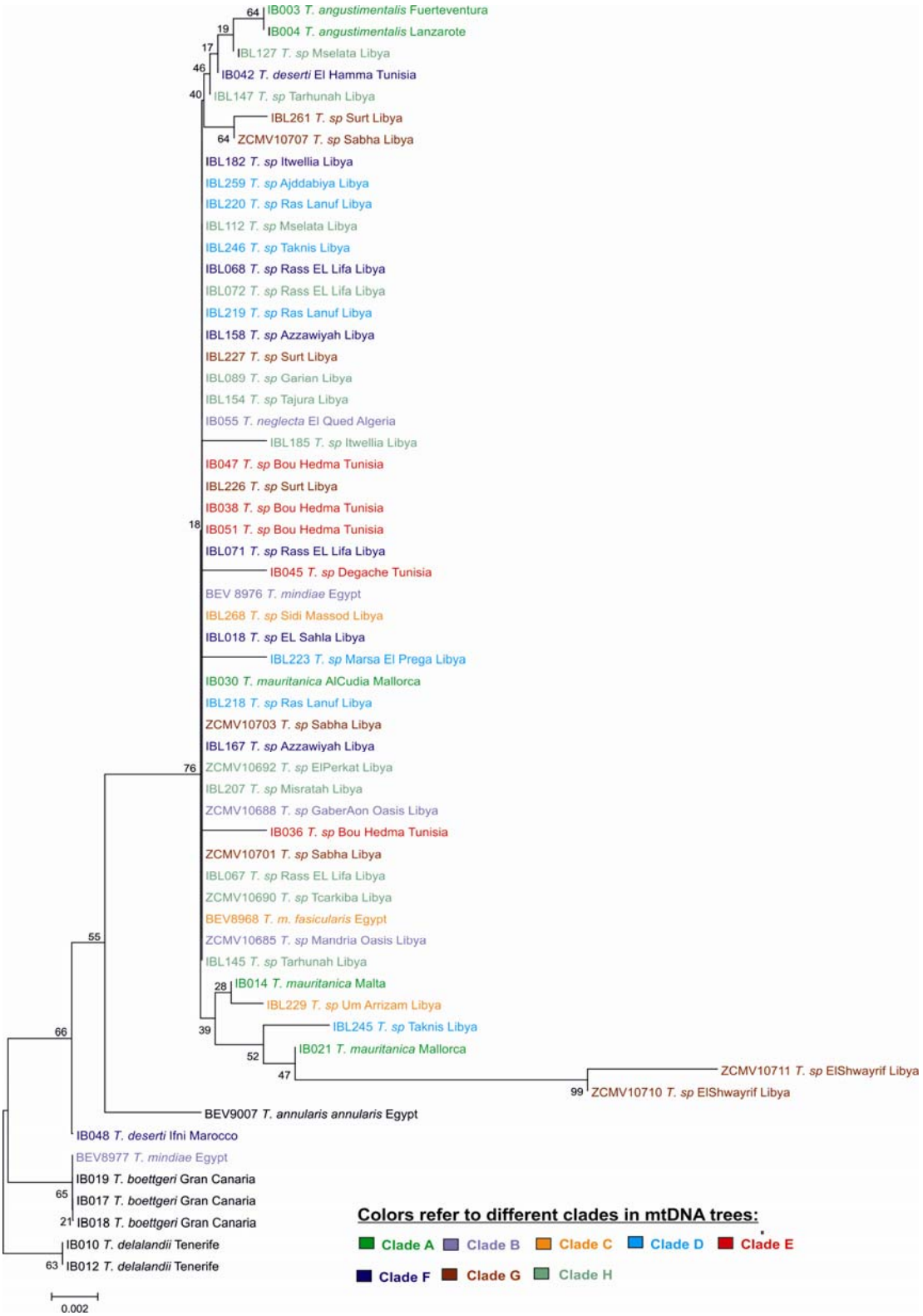


Figure 44. Neighbor-Joining phylogenetic tree based on 361 bp Phosducin sequence; depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup. Values near the branches correspond to bootstraps values based on 1000 pseudoreplicates.

3.3.7. Phylogeny based on Rag2 nuclear gene sequence data

The study includes 59 specimens of genus *Tarentola*, of which 57 are ingroup, and two specimens of *T. delalandii* were designated as outgroup. Data consisted of a total of 387 aligned nucleotide positions of Rag2. The average of nucleotides frequencies was: f (A) = 0.32, f (C) = 0.17, f (G) = 0.24, f (T) = 0.28. Out of 387 characters, 19 (4.9%) were variable and 9 (Pi: 2.3%) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the results were largely congruent and supported the same tree topology. HKY+I model of molecular evolution was chosen by Modeltest ver. 3.7 and Mrmodeltest ver. 2.3 respectively, under the Akaike Information Criterion.

Neighbor Joining analysis was carried out using MEGA ver.4.1. For calculating of gaps/ or missing data positions, pairwise deletion option was selected. Jukes-cantor model of molecular evolution as implemented in MEGA program was chosen. To provide support for the resulting tree, bootstrap support values were calculated from 1000 replicates (Figure 45).

A Bayesian analysis was carried out using Mr.Bayes Ver.3.1. The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 1.5×10^{6} generations, and saving tree in each 100^{th} generation using a HKY+I model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (3750 samples) from the burnin were discarded. The remaining trees were combined, and a 50% majority consensus tree was generated (see appendix 7).

The maximum likelihood (ML) analyses were performed using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics platform, CNRS – Université Montpellier II. The best-fit model (HKY+I) was

determined by Modeltest ver. 3.7, we used HKY85 model of evolution as implemented in PhyML program, and maximum likelihood searches were performed with a heuristic search. To provide support for the resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping (see appendix 8).

The trees were uninformative, with different degree of statistical support and comprised unresolved trees topology.

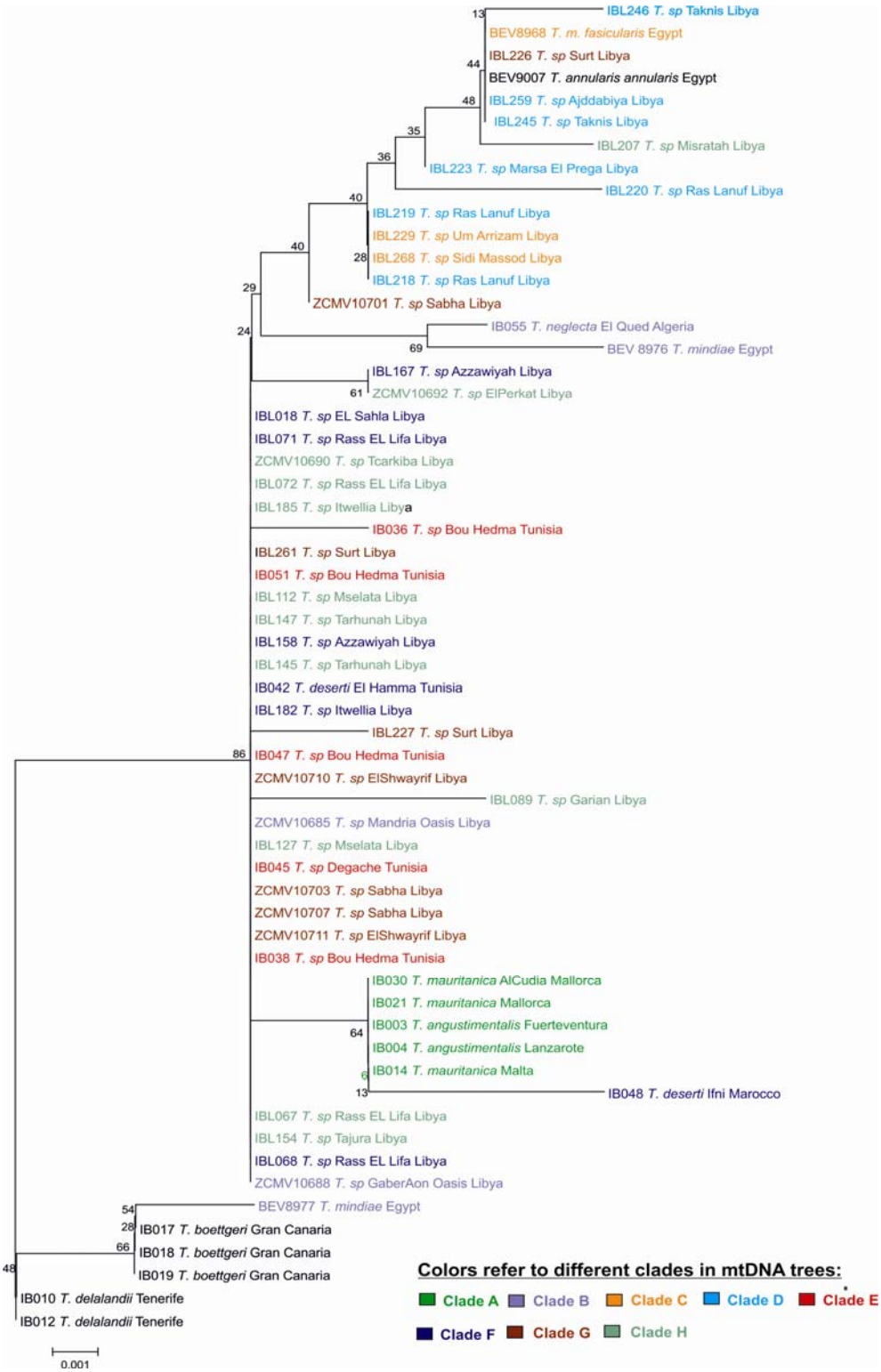


Figure 45. Neighbor-Joining phylogenetic tree based on 387 bp Rag2 sequence; depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup. Values near the branches correspond to bootstraps values based on 1000 pseudoreplicates.

3.3.8. Phylogeny based on combined nuclear genes sequence data

The study includes 59 specimens of genus *Tarentola*, of which 57 are ingroup, and two specimens of *T. delalandii* were designated as outgroup. For increased resolution with more positions, we combined the three nuclear genes, the final dataset consisting of 1172 aligned nucleotide positions of nuclear DNA (424 bp *C*-mos, 261 bp Phosducin, and 387 bp Rag2). The average of nucleotide frequencies was: f (A) = 0.29, f (C) = 0.20, f (G) = 0.24, f (T) = 0.27. Out of 1172 characters, 59 (5%) were variable and 29 (Pi: 2.5%) of these parsimony informative. Neighbor Joining analyses, Maximum likelihood analyses and Bayesian analyses were used, the results were largely congruent and supported the same tree topology. TVM+I and GTR+I models of molecular evolution were chosen by Modeltest ver. 3.7 and Mrmodeltest ver. 2.3 respectively, under the Akaike Information Criterion.

Neighbor Joining analysis was carried out using MEGA ver.4.1. For calculating of gaps/ or missing data positions, pairwise deletion option was selected. Jukes-cantor model of molecular evolution as implemented in MEGA program was chosen. To provide support for the resulting tree, bootstrap support values were calculated from 1000 replicates (Figure 46).

A Bayesian analysis was carried out using Mr.Bayes Ver.3.1. The Bayesian posterior probabilities were estimated using a Metropolis-coupled, Markov chain Monte Carlo (MC-MCMC) sampling approach. Both runs started with random starting trees, run for 10×10^6 generations, and saving tree in each 1000^{th} generation using a GTR+I model of evolution as determined by Mrmodeltest ver. 2.3. In both searches, the stationary of the Markov chain was determined as the point when sampled log-likelihood values plotted against generation time reached a stable mean equilibrium value. 25% of the samples (2500 samples) from the burnin were discarded. The remaining trees were combined, and a 50% majority consensus tree was generated (Figure 47).

The maximum likelihood (ML) analyses performed using PhyML ver. 3.0 online program (http://atgc.lirmm.fr/phyml/) from Montpellier bioinformatics platform, CNRS – Université Montpellier II. The best-fit model (TVM+I) was determined by Modeltest ver. 3.7, we used GTR model of evolution as implemented in PhyML program, and maximum likelihood searches were performed with a heuristic search. To provide support for resulting maximum likelihood tree, bootstrap support values were calculated from 1000 replicates of heuristic searches, with NNI swapping (Figure 48).

Our analyses of 1172 aligned nucleotide positions of nuclear DNA result a robustly supported Bayesian topology and moderately supported ML topology. Both trees are uninformative and included unresolved tree topology.

Somewhat unexpectedly, the analyses for each nuclear gene partition or combined nuclear genes do not support the majority of the mtDNA lineages (phylogenetic relationships). With the exception of *C*-mos and Rag2 where group *T. neglecta* from Algeria and South Libyan oases linked together with *T. mindiae* from Egypt.

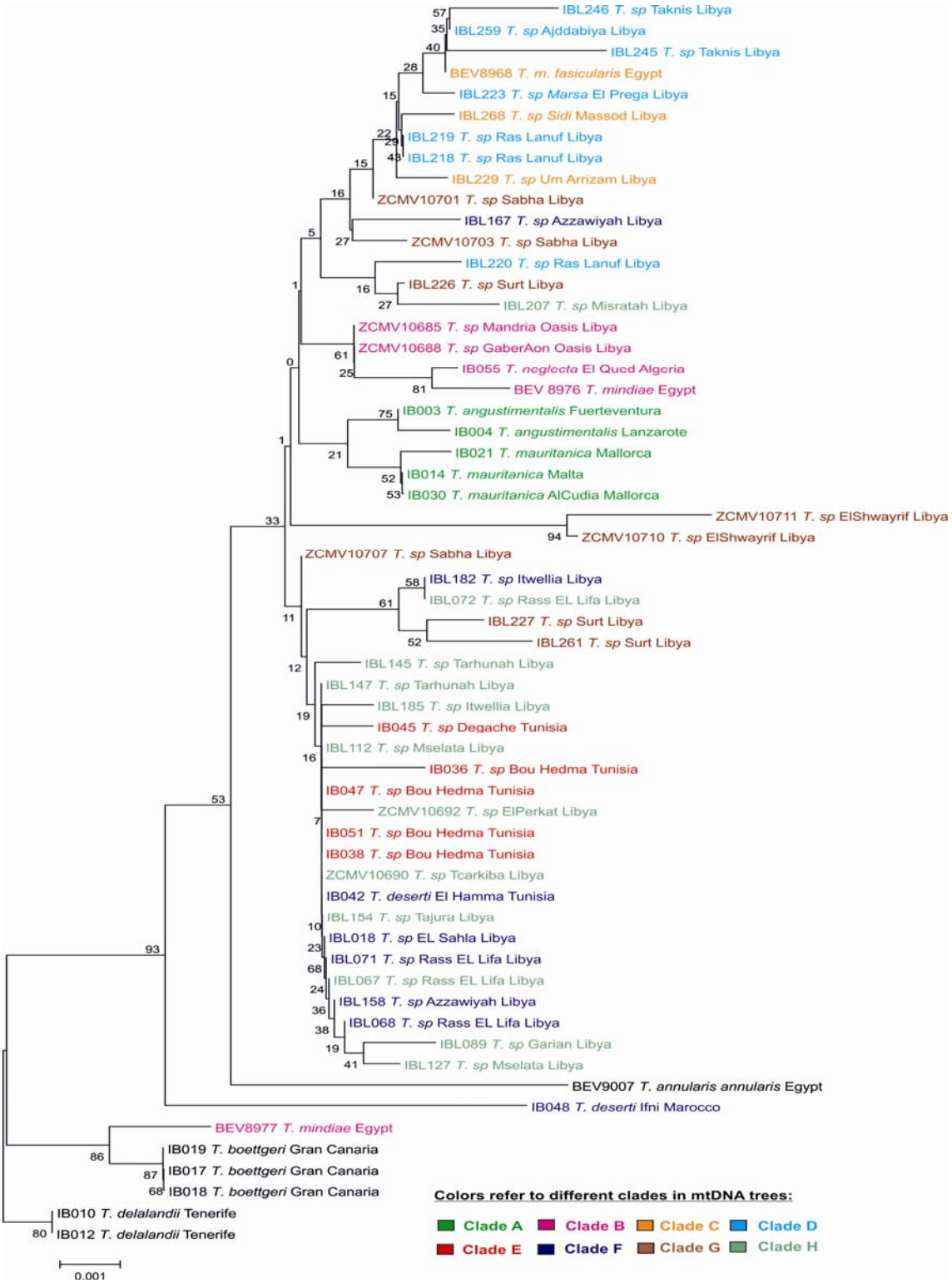


Figure 46. Neighbor-Joining phylogenetic tree based on 1172 bp nuclear DNA sequence; depicting the relationships among haplotypes, with *Tarentola delalandii* as outgroup. Values near the branches correspond to bootstraps values based on 1000 pseudoreplicates.

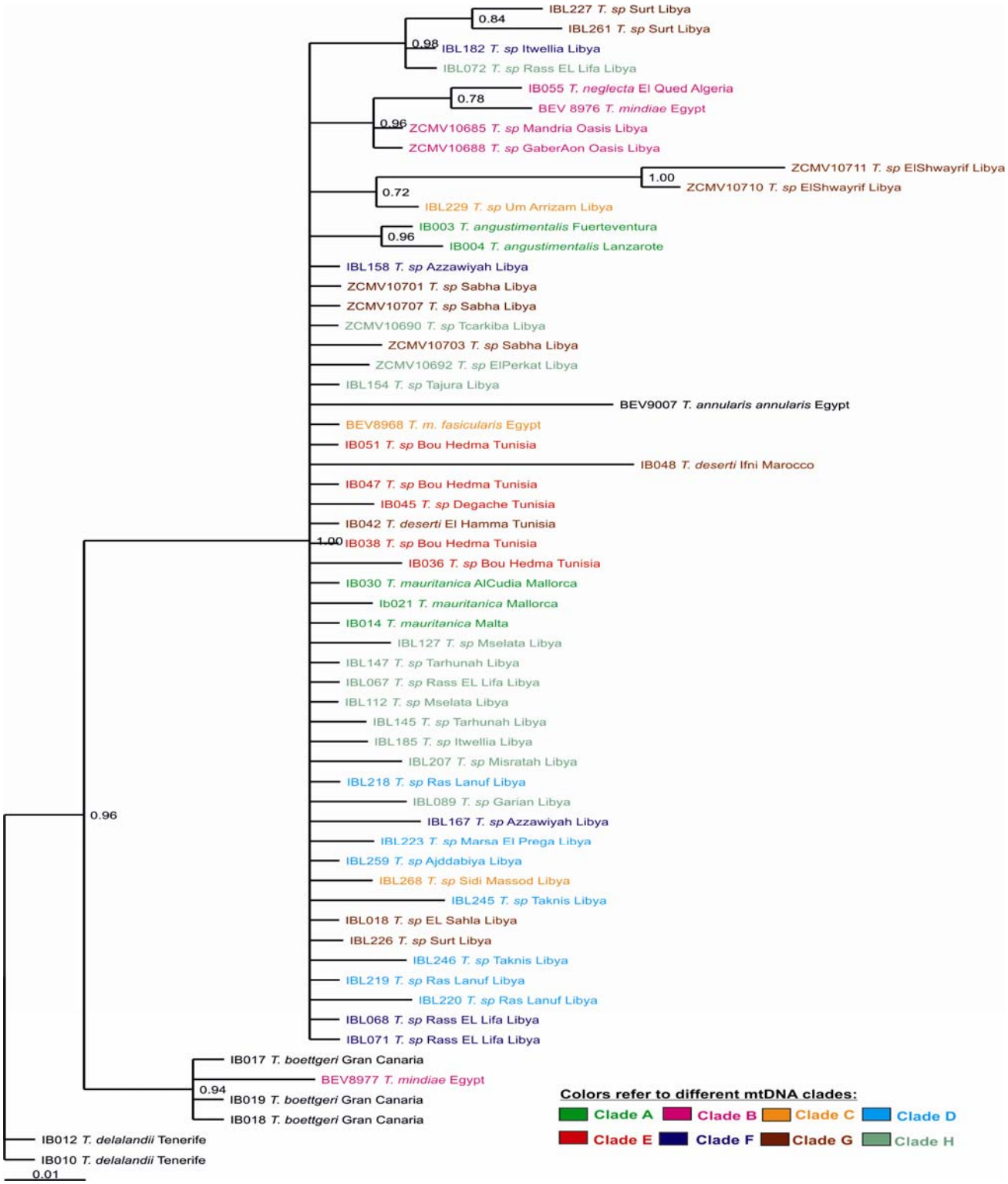


Figure 47. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on 1172 bp nuclear DNA sequence, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.

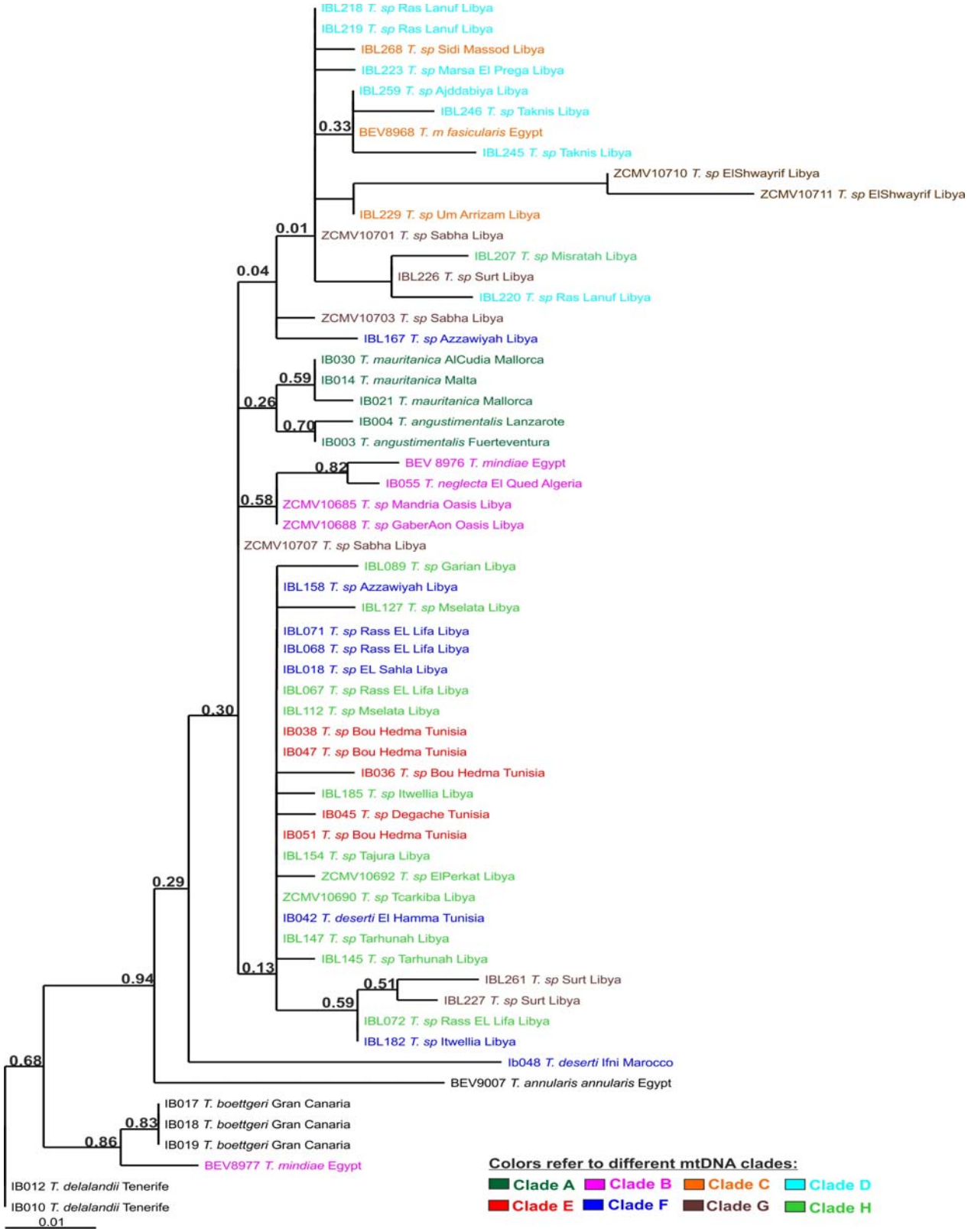


Figure 48. Tree derived from ML analysis using the model explained in the text, based on 1172 bp nuclear DNA sequence. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.

04 GENERAL DISCUSSION

This work represents a significant study of the patterns of intrageneric diversity and systematics in genus *Tarentola* in North Africa (Morocco, Algeria, Tunisia, Libya and Egypt), in Saharan and coastal areas. Previous studies (Geniez et al, 1999; Carranza et.al, 2002; Harris et al, 2003; Harris et al, 2004; Perera and Harris, 2008; Harris et al, 2009; Rato et.al, 2010) have been limited to a small distribution range involving many Moroccan populations but largely neglected Algerian , Tunisian, Libyan and Egyptian populations, and have never included a sufficient range of samples to make reliable conclusions about relationships, evolution, geographical distribution and observe, if new species or subspecies within genus *Tarentola* in this region can be identified. In order to investigate some general aspects about the taxonomy, relationships, evolution and geographic distribution of genus *Tarentola* in this area, this work is extended here by including extensive material from Libya as well as from the rest of North African countries (Morocco, Algeria, Tunisia and Egypt). For the samples collected from Libya; for the first time the samples were collected from such a broad geographical range of the country, which have never previously been analysed. In this study phylogeny and phylogeography of different populations of the genus*Tarentola* in North Africa were investigated, we used both molecular and morphological techniques. The comparison of the results with each other and with results from other North African reptile groups allow the deduction of more robust conclusions about complex patterns of descent and divergence relationships.

4.1. Morphological comparisons among N-African *Tarentola*

The morphological analysis of North African *Tarentola* populations in this study reveals a high degree of morphological differentiation corresponding to geographic distribution. T-test, Mann-Whitney (U-test) and One-Way ANOVA analyses demonstrated that Libyan populations are significantly different among

each other by at least some of the characters, as well as differing from all North African groups by at least some of the characters. Linear discriminant function analysis (LDFA) and Principle component analysis (PCA) suggested six broadly distinct morphological lineages /or clusters occurring in North Africa:

First, group of North African *T. mauritanica* from Morocco, Algeria and Tunisia. Second, North African *T. deserti* group from Morocco, Algeria and Tunisia. Third group comprises specimens called *T. sp*-complex from Tripolitania (north-west Libya), a group identified as *T. deserti* from Tripolitania, other identified as *T. m. fascicularis* from Cyrenaica Libya, *T. sp* from Suirt in central-northern Libya and *T. sp* from south-central Tunisia. Fourth group contains *T. sp* from Ras Lanuf in north-eastern Libya and *T. sp* from Aljabal Alakhdar in north-eastern Libya. Fifth group consists of Sahara desert specimens *T. sp* from Sabha. And sixth, a small number of specimens from restricted localities from isolated Sahara desert oases in southwestern Libya, these samples identified as *T. neglecta*.

1- North African *T. mauritanica*

Several specimens of *T. mauritanica* from North Africa (Morocco, Algeria and Tunisia) were morphologically studied; the statistical analysis of morphological characters did not show any significant difference between these groups (see tables. 6, 7, 8 and 9), all three groups are grouped closely together in CDF and PCA plots. Despite these overlaps, it is possible to distinguish them from each other in CDF plots (see figure. 22). In contrast, the three groups showed an extensive overlapping in PCA plots (see figure. 29).

2- North-West African *T. deserti*

North-West African *T. deserti* are distributed geographically from south-eastern Morocco through Algeria to southern Tunisia, this group was clearly differentiated in some morphometric and meristic characters from all other groups in this study, it is characterized by significant features: i,e., they have high number of scales and lamellae underneath the first, fourth and fifth toes (12-14, 17-20 and 22-24 respectively); high number of gular scales (49-63);

the hindlimb length is big 22.1-43.1 mm in males; the distance between ear openings up to the mental is 13.3-23.5 mm in males. When NW-African populations of *T. deserti* are compared with all other groups in this study, they form a clear discrete group, with no overlap with any other groups in CDF and PCA plots (see figures. 21 and 28).

3- Libyan group (*T. sp*-complex, *T. deserti*, *T. m. fascicularis*, *T. sp*-Suirt) and south-central Tunisian *T. sp*.

Specimens originating from a wide area in Libya: *T. sp*-complex and *T. deserti* from Tripolitania (north-western Libya), *T. m. fascicularis* from Cyrenaica (north-eastern Libya), *T. sp* from Suirt (central-northern Libya); and southern Tunisian *T. sp*. All these specimens showed a kind of affinities in CDF and PCA plots (see figures. 21 and 28), because as we know these geckos are largely indistinguishable depending on external appearance; however, we can distinguish them from each other (despite the slight overlapping between them). There are significant differences between these groups in a number of characters: i,e., Libyan *T. deserti* has more ventral scales than *T. sp*-complex, *T. sp* (Suirt) and *T. m*. fascicularis; *T. m. fascicularis* has low number of scales and lamellae underneath the first, and fourth toes when compared with *T. sp* complex, *T. deserti* and *T.sp* Suirt*; T. sp* Suirt have higher numbers of scales and lamellae underneath the fourth toe than all other specimens in this group; *T. sp* of south-central Tunisia are consistent with Libyan group *T. sp* complex, *T. deserti* and *T. m. fascicularis* in the terms of having more or less the same number of scales and lamellae underneath the first, fourth and fifth toes, but differ from these group by a low number of ventral scales. However, the south-central Tunisian populations (*T. sp*) share a mixture of morphological characters with either *T. deserti* or *T. m. mauritanica,* e.g. their size is smaller than deserti, whereas body and eye colour are close to *deserti* (Joger, 2003). And (*T. sp* Tunisia) differ from *T. deserti* as well as from Libyan *T. sp*-complex, it was noted that they show pattern of divergence in CDF plots (see figure 21); this is true also for Libyan

T. deserti and North African *deserti,* these size and scalation linked characters could be locally favoured by environmentally triggered selection, as these two groups live in different environmental conditions, Libyan *deserti* distributed in northern Tripolitania, in Mediterranean climate; while North-African *deserti* live in desert regions.

4- Libyan group (*T. sp*-Ras Lanuf and *T. sp*- Aljabal Alakhdar) from Cyrenaica

T. sp from Ras Lanuf is a giant lizard, characterized by its very large size (SVL up to 96.36 mm, their size is bigger than *T. deserti*) with long and broad head, but body and eye colour are close to *T. m. fascicularis,* the geographic extent of this gecko in the desert coast area of Ras Lanuf and Marsa El Prega in north-eastern Libya*.* However *T. sp* of Aljabal Alakhdar is somehow smaller in size, and endemic to Aljabel Alakhdar area, which is covered with green forest. Morphological study of external characters showed that these geckos (*T. sp* Ras Lanuf and *T. sp* Aljabal Alakhdar) significantly differ in some morphological features from all other groups in this study (see tables. 6, 7, 8 and 9), and as well as from each other. They cluster with each other in CDF and PCA plots, but it is possible to distinguish them from each other, despite the overlapping between them (see figures. 24, 30 and 33).

5- Libyan southwestern Sahara desert group

This group is composed of specimens of *T. sp from* Sabha province in southern Libya. Morphological analysis of external features suggests only one major morphologically distinct group. Previous herpetological studies in southern Libya (Ibrahim, 2008) assigned morphologically this group to *T. m. mauritanica.* However*,* our morphological analysis confirms that this group is not related to *T. mauritanica* or any known species or subspecies of North African *Tarentola*, since it does not cluster with any known groups in CDF and PCA plots, however, the collected samples in this study possess

significant morphological features which distinguish it from the other groups. The statistical analysis (T-test, Mann-Whitney U test, and One-Way ANOVA) showed significant difference between this group and all other groups in this study, in a number of characters: i,e., they have a high number of scales and lamellae underneath the first toe, more than all groups in the study excluding *T. deserti* (North Africa) which has the same number; also a high number of scales and lamellae underneath the fourth toe, excepting North African *T. deserti* and Moroccan *T. m. juliae* which have more or less the same number; a high number of ventral scales, excluding *T. boehmei* which has more ventral scales; and a high number of dorsal tubercles. These high numbers of scales are thought to be an adaptation to the specific habitat niche (Sahara desert climate). In CDF and PCA plots, this group (*T. sp* Sabha) forms a clear discrete group, with no overlap with any other groups (see figures. 26, 27, 32 and 33).

6- Libyan southwestern Sahara desert oases group

This group is composed of a small number of samples, collected from isolated Sahara desert Oases, in Libyan south-western Sahara (Gaber Aown oasis and Mandria oasis), they form only one major morphologically distinct group in CDF and PCA plots (see figures. 27 and 33). Morphologically this group is assigned to the species *T. neglecta,* as they have small size and the same color patterns (light gray-brown color, with dark brown near-parallel bands in the dorsal region from the top head to the tail) as *neglecta*. However, it is clearly differentiated at least in some morphological features from all other groups in this study, also from the two known subspecies of *T. neglecta* (Northern Sahara *T. n. neglecta* Strauch, 1895 and Central Sahara *T. n. geyri* Joger, 1984). Our samples are characterized by a low number of scales and lamellae underneath the first, fourth and fifth toes, they have the same number of scales and lamellae underneath the fourth and fifth toes (15, 18 respectively), more or less as in *T. n. geyri* (Joger, 1984a); a low number of interorbital scales (12-13), consistent with *T. n. geyri*; they have 110 scale

rows around the midbody, more than *T. n. neglecta* and *T. n. geyri*, which have 72-98 and 93-102 respectively; a high number of gular scales (42-52), more than *T. n. neglecta* and *T. n. geyri*, which have 29-41 and 38-40 respectively. From all these features, in addition to the small size of our specimens (SVL up to 34.76 mm), which is smaller than *T. n. neglecta* and *T. n. geyri* (59 mm, 50 mm respectively), there is a high probability that these specimens from south-western Sahara should to be a new subspecies of *T.neglecta*.

4.2. Molecular phylogenetic affinities among N-African *Tarentola*

Geckos of the genus *Tarentola* are distributed in North Africa, from Morocco to Egypt. The relationships among *Tarentola* recovered in this work using mitochondrial genes and different phylogenetic reconstruction methods, yield almost identical topologies with generally high statistical support, indicating the robustness of phylogeny and efficiency of the marker genes as powerful molecular tools. The statistical support (bootstrap and posterior probabilities) of reconstructed phylogenies in this study in general lies within a moderately to highly reliable range. Such support values are considered to be good indicators of the robustness of branches in the reconstructed phylogenetic trees. All individual as well as combined phylogenetic analyses of mtDNA dataset (12srRNA and two-fragment16srRNA) reveal a set of well resolved clades, no conflicted topology among partitions were observed. ML and Bayesian topologies were largely concordant. In the light of our results, it is surprising that such a substructure and high genetic divergence was found between mtDNA lineages. These are not confirmed by the nDNA genes (C-mos, Rag2 and Phosducin); the nDNA data do not support the majority of the mtDNA clades. Such results suggest an incomplete lineage sorting of these nuclear markers. Which means that, despite the highly divergent mtDNA lineages, the nuclear genome is not as distinct in the different clades. This lack of population structure in nuclear genealogies with highly differentiated mtDNA lineages is not, however, uncommon, and has been already detected in many reptile species such as

Podarcis (wall lizards) and (dark green whip snake) *Hierophis viridiflavus* (Pinho et al., 2007; Rato et al., 2009). Based on our analysis of mtDNA dataset, we confirm the existence of eight monophyletic groups in this range, most of which have some geographical consistency (Figure 41). Phylogenetic structure among these groups support some of the conclusions reported in previous studies (Harris et al, 2004a 2004b, 2009; Rato et al, 2010), in particular, demonstrating once again the paraphyly of *T. mauritanica* with respect to *T. angustimentalis* as well as the presence of two evolutionary lineages in Lampedusa Island and Conigli Islet (Italia), one lineage is nearly identical to specimens from Libya. Taking into account the high genetic variability of genus *Tarentola* in North Africa, and the typical morphological homogeneity of this group, it is thought that this could be a cryptic species complex. However, according to the dataset obtained from the samples collected from different localities in North Africa (Morocco, Algeria, Tunisia, Libya, and Egypt), several novel evolutionary relationships between the different new forms were recovered, different mitochondrial lineages were found and could be hypothesized:

1- According to our analysis, there is agreement about the monophyly of a group (clade F) in all individual and combined mtDNA trees. This group is composed of one specimen of *T. deserti* from Tunisia and several specimens of *Tarentola* from Tripolitania. The Libyan group appears so far only in the north-western regions of Tripolitania. These specimens are assigned to the *deserti* group, this is because the divergence among all these taxa and also *T. deserti* from Tunisia is very low, it ranges between 0.2%-0.6% (uncorrected genetic distance in 12srRNA).

2- A Saharan desert clade (B) is subdivided into two groups; the first includes two specimens of *T. mindiae* form Egypt, which form a monophyletic clade with the second group, which is composed of three specimens, one specimen of *T. neglecta* from Algeria and two specimens from southern-Libyan Sahara Oases which are assigned morphologically to the *neglecta* group. The three specimens of *neglecta* are nearly genetically identical in

this region of mtDNA. The uncorrected genetic distance between the two subclades (*mindiae* and *neglecta*) is 5%.

3- Our mtDNA phylogenetic results prove the existence of *T. m. fascicularis* in Aljabal Alakhdar area (Cyrenaica-Libya), the mtDNA trees support the monophyly of *T. sp* from Um Arrizam, Sidi Massod (Aljabal Alakhdar) and one specimen of *T. m. fascicularis* from Egypt. *T. m. fascicularis* from Egypt form the basal lineage of this group; the uncorrected genetic distance between Egyptian *fascicularis* and Libyan samples in this group (clade C) is very low.

4- Mitochondrial DNA analysis supported the monophyly of a lineage made up of specimens of *T.sp* from north-eastern Libya (clade D); this clade is divided into two subclades. One consists of specimens of *T. sp* which is distributed in the coastal plain of Ras Lanuf and Marsa El Prega, and the other consists of specimens of *T. sp* collected from a mountain area at Aljabal Alakhdar (namely from Taknis). The uncorrected genetic distance between these two subclades is about 2% for 12sRNA. Based on the combined mtDNA, the uncorrected genetic distance between this group (clade D) and *T. m. fascicularis* is 7%; lower that between this clade and *T. deserti* or *T. m. mauritanica* (8% and 12% respectively). This supports the view that, although *T. sp* from Ras Lanuf is more closely related morphologically in at least some characters to *deserti*, but phylogenetically it is more closely related to *fascicularis*.

5- Phylogenetic analysis of mtDNA supported the monophyly of *T. sp* from Sabha province (south-western Sahara desert), which form a sister lineage to *T. sp* from Suirt (north-central Libya, Suirt basin). These two groups (clade G) are separated geographically from each other by about 560 km, by a range of scattered mountains (such as Jabal al Sawda, Jabal al Hassawinah and Jabal Al Haruj al Aswad) and valleys (dry wadis) or ditches (such as Hun ditch), which constitutes a sizeable barrier to exchanges between northern and southern populations, yet the

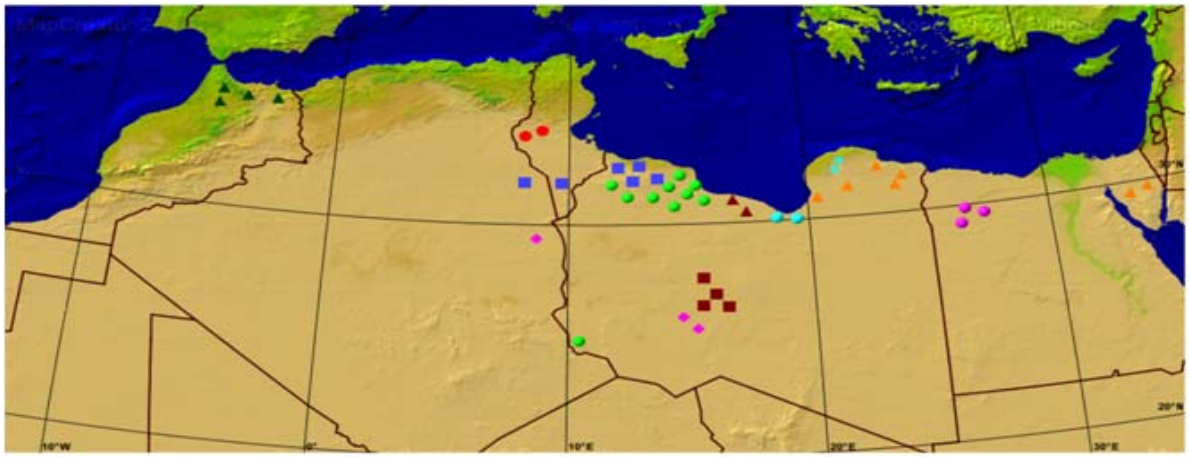
divergence between these two groups is 2% only in the 12srRNA (uncorrected genetic distances). Previous studies in southern Libyan Sahara (Ibrahim, 2008) assigned the Sabha group to *T. m. mauritanica*. However, our mtDNA analysis indicates that, Sabha and Suirt populations are not closely related to *mauritanica,* but are more closely related to *deserti* and *fascicularis* than to *mauritanica.* Based on the combined mtDNA, the uncorrected genetic distance between clade G (central-Libyan group and south-Libyan group) and *T. deserti* are (5%) lower than between the clade G and *T. m. mauritanica* (11%). This supports the view that despite some morphological similarity, undescribed *T. sp* from Sabha and central-Libyan *T. sp* are not subspecies of *T. mauritanica.*

6- mtDNA sequences stresses the monophyly of south-central Tunisian *T. sp* (clade E) in all individual and combined analysis. Previous electrophoretic studies (Willand, 1997; Joger et al, 1998) showed that, the blood plasma protein alleles of this gecko are distinct and shared by neither *T. mauritanica* nor *T. deserti*. Our mtDNA results show that, south-central Tunisian gecko do not cluster with *T. mauritanica* but with undescribed *Tarentola* from Libya, in particular with the most north-western ones. The uncorrected genetic distance between undescribed Libyan *Tarentola* and south-central Tunisian *T. sp* is lower than between this clade (E) and *T. mauritanica* (see Table 17).

7- The mtDNA analysis supports the monophyly of clade (H), this group forms a robust monophyletic assemblage that is further subdivided into the population from Tripolitania (namely: Itwellia, Tajura, Msalleta, Tarhunah and Misratah); and the population from south-western Libya (namely: Tcarkiba and El Perkat); and the western mountain group (Rass El Lifa and Garian), the divergence among all these subclades is relatively low. In the mtDNA trees, this group (clade H) is aligned more closely with group *deserti* and *fascicularis* than with group *mauritanica*, uncorrected genetic distance between clade H and group *deserti* (clade F) and

fascicularis (clade C) is lower as than between clade H and *mauritanica* (clade A). It was 6%, 7% and 11% respectively.

8- Depending on the results which were acquired from the 12sRNA analysis, the recently discovered Lampedusa and Conigli Islands *Tarentola* (Harris et al, 2009) can be separated in two lineages. One lineage is closely related to undescribed Libyan *T. sp*-complex from Tripolitania (which were not included in previous studies); based only on the 12srRNA, the divergence among *T. sp*-complex and the Italian group ranges between 0.4%-2% (uncorrected genetic distances), and all compose one clade (H). And the other one seems to be nearly identical to the recently described *T. fascicularis wolfgangi* (Joger and Bshaena, 2010) from central-Tunisia (based only on the 12srRNA, the divergence between these two groups ranges between 0.1%-2%), which all together form clade E. These results represent a recent divergence, and confirm that, Lampedusa and Conigli lineages were probably introduced from North Africa through two distinct colonization events, from Tripolitania and central-Tunisia, either by natural rafting or anthropogenic introduction. Such events are known widely within gecko genera (see: Carranza et al, 2000), and also by other reptiles e.g. *Chaldides c. vittatus*, which reached Sardinia Island more recently from northern Africa (Tunisia), possibly by anthropogenic introduction (Carranza et al, 2008); this is also true of *Chalcides ocellatus* and Viperine snakes *Natrix maura*, in which the population of Italian Island (Sardinia) also has its closest relatives in North Africa (Giovannotti et al., 2007; Guicking et al., 2003).



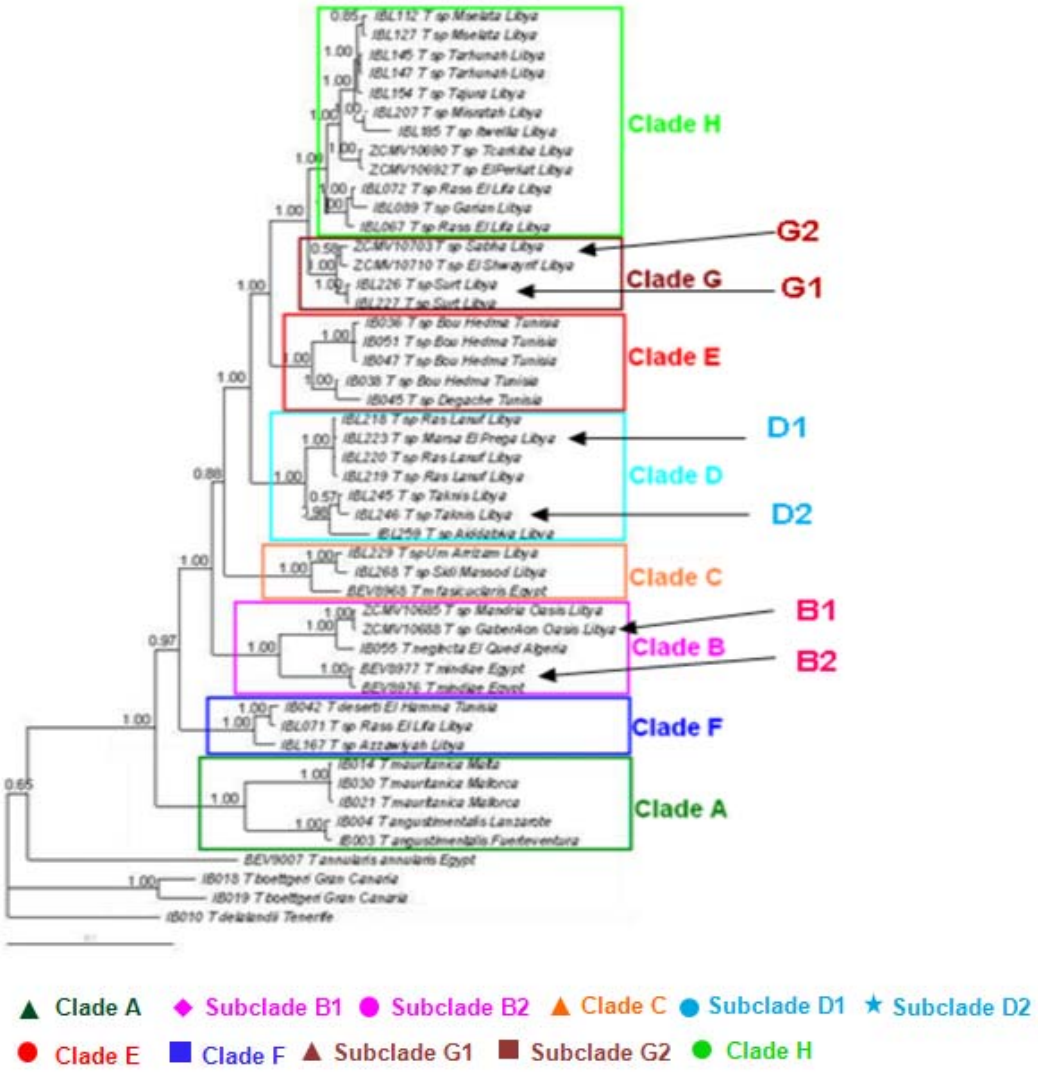


Figure 49. 50% majority-rule tree consensus obtained from Bayesian MCMC analysis, based on 1433 bp mtDNA sequences , and the map above illustrates the distribution of clades geographically

4.3. Genetic distances

The high level of genetic divergence found within geckos is typical. Our results are another example of high genetic variation within North African *Tarentola*. Most lineages in this study are highly genetically differentiated (Table 17). The genetic variation between these lineages is far higher than typically found within other reptile species. Previous studies in North African *Tarentola* (Harris et al., 2004) show that, the genetic distance in 16srRNA between North and South Morocco population was 5%, whilst between samples from northeastern Libya and those from northwestern Tunisia it was over 8%. Another phylogenetic study (Brown et al., 2002) about *Agama* lizards in Morocco shows that, the maximum intraspecific sequences variation for the same region of 16srRNA was 2.6%, ‘‘this variation was considered high and represents one of the most substantial within-species divergences described at that time’’. On average geckos appear to have higher levels of mtDNA divergence between species than other lizards (Harris, 2002). Several another studies have indicated intraspecific variation in different gecko groups far higher than is typically seen between species of vertebrates (e.g. Lamb and Bauer, 2000, 2002). Jesus et al. (2002) studied the mtDNA variation among different *Tarentola* forms from the Cape Verde islands and found that the mtDNA variation was high between species relative to other reptiles from the same islands.

Table 17. Uncorrected ‘‘P’’ distance between main clades, estimated of evolutionary divergence between sequences, based on pairwise analysis of 1433 bp mtDNA sequences

	Clade A	Clade B	Clade C	Clade D	Clade E	Clade F	Clade G	Clade H	Outgroup
Clade A									
Clade B	0.0921								
Clade C	0.0972	0.0704							
Clade D	0.1180	0.0977	0.0692						
Clade E	0.1052	0.0853	0.0562	0.0705					
Clade F	0.0974	0.0634	0.0630	0.0802	0.0645				
Clade G	0.1145	0.0873	0.0662	0.0665	0.0694	0.0510			
Clade H	0.1141	0.0886	0.0691	0.0711	0.0706	0.0578	0.0270		
Outgroup	0.1234	0.1407	0.1357	0.1545	0.1564	0.1422	0.1531	0.1490	

4.4. Definition of species

Since before Darwin, there has been debate and disagreement about the meaning of the word ‘species’. Darwin himself documented the fact that there were multiple definitions of this word among naturalists (Darwin, 1859). However, there is a distinct lack of consensus among biologists concerning the optimal definition of a ‘‘species’’ or the operational criteria for their delimitation. During the last 70 years, many new species concepts have been formulated (e.g. the biological species concept by Mayr (1942), the evolutionary species concept by Simpson (1951), and the ecological species concept by Van Valen (1976)); about 24 different named species concepts are known (Mayden, 1997). Much of the argument surrounding the debate has been over hypothetical concepts versus practical concepts (specifically, concepts with specific species identification criteria). De Queiroz (2007) devises the ‘‘General lineage concept of species’’, he proposes that, there is a common element among all contemporary species concepts and suggests a unified species concept in which species are ‘‘separately evolving metapopulation lineages, or more specifically, segments of such lineages’’. In this concept De Queiroz separates the issue of species concept from species delimitation, where boundaries and numbers of species are inferred. In the view of De Queiroz, most of the divergences between contemporary species concepts arise in the criteria they assign to recognizing species and the point in which diverging lineages can be considered separate species. Therefore, the general consensus seems to be that members of a species have an evolutionary history more similar to members in the same species than they do with other species (Hey, 2006). Despite the controversy surrounding species concepts, there is a tendency to separate species identification and delimitation from the more conceptual aspect and to focus only on identification (operational) criteria. However, the operational criteria used in species delimitation have also come under scrutiny. Today DNA sequence data are commonly used to infer species boundaries, although most species continue to be identified based on morphological descriptions. Indeed, several authors

have stressed the importance of examining multiple different characters in order to gain evidence for the existence of separate species. The concordance of characters (e.g. morphological characters, genetic data) can form crucial evidence on which species status decisions are made (Avise and Ball, 1990; Joger et al, 1998).

As discussed above, the general lineage concept, equates species with population level segments of evolutionary lineages, speciation is seen as a gradual process and the multitude of species delimitation criteria represent events along the process. As such, there is no one definitive criterion which can be used to determine the species status of a population; instead, De Queiroz requested use of multiple criteria in the delimitation of species. This approach in species identification is concordant with the Integrative taxonomy approach proposed by Padial et al. (2010), which also advised to use multiple criteria in the identification of species. Accordingly, in this thesis, we have adopted this approach in identification and delimitation of different species and subspecies of gecko *Tarentola* in North Africa following these current criteria:

1- Isolation and recognition (Mayr, 1963) criteria, reproductive isolation of species, evidenced by a lack of intergradations of phenotype with species separated by clear disjunction.

2- Phenetic cluster criterion, which distinguishes species as separated clusters in multivariate analysis (Sokal & Sneath, 1963).

3- Diagnosiability criterion, where species show unique sets of primitive and derived characters; at least, a population must demonstrate a fixed difference in one or more characters (Cracraft, 1989).

4- Apomorphy criterion, a species must possess entirely unique derived characters, these may be morphological or molecular genetics characters.

Species are therefore defined by a mixture of isolation, monophyly (phylogeny) and phenetic differentiation.

4.5. Conclusions of morphological and molecular study

Parapatric or sympatric occurrence of mitochondrial clades could be interpreted in different ways; either different biological species or even co-existence of two mitochondrial lineages in a mixed interbreeding organismal population. Depending on the results obtained from both morphological and molecular study; in the case of *T. deserti* population in Tripolitania (north-west Libya), there is evidence of the former explanation, as the molecular differences coincide with morphological differences. When a conservative two-species concept (*T. mauritanica* - *T. deserti*) is applied, all individual and combined mtDNA trees show without doubt that all sequenced Libyan OTUs, south-central Tunisian OTU, and Egyptian OTU are closer to *T. deserti*, and not to *T. mauritanica*. Undescribed Libyan *Tarentola*, these populations form several geographically restricted, monophyletic clades; the most northwestern ones are sister to *T. sp* from south-central Tunisia. Also *T. m. fascicularis* from Egypt and north-eastern Libya, and even *T. neglecta* and *T. mindiae* appear more closely related to Libyan populations. It is noteworthy that the populations near the neo-type locality of *T. m. fascicularis*, in north-eastern Libya (Cyrenaica), belong to a separate clade (clade D).The mitochondrial genetic distance between the Libyan clades, the south-central Tunisian clade, the Egyptian *T. m. fascicularis* clade and *T. deserti* are lower than between all these clades and *T. mauritanica* (see table 17). This supports the view that despite the affinity in some morphological characters (with *mauritanica*), the Libyan, Tunisian and Egyptian clades are not subspecies of *T. mauritanica.* On the other side, assigning these OTUs to *T. deserti* would, however, create a paraphyletic *T. deserti*, with *T. neglecta* and *T. mindiae* which are certainly separate species within *T. deserti*. In this case the most parsimonious taxonomic explanation/ or solution with regard to the mitochondrial cladograms is to subsume clades C, D, E, G, and H under one separate species *T. fascicularis*. Morphological investigations show that several of the mitochondrially defined populations, in particular if they occur in desert

areas (Sabha in south-west Libya, Tunisia and Algeria but not Libyan *T. deserti*, and also a subclade of clade D) can be distinguished by larger size and higher scale counts. These size-linked characters could be locally favoured by environmentally triggered selection. On the other hand, morphological dissimilarity does not preclude genetic proximity, and genetically distant clades may share morphological similarity.

From comparing all mtDNA phylogenetic trees that have been obtained in this study, a reliable phylogeny was obtained from analysis of a combined mtDNA dataset by Bayesian approach. Our decision was relying on the Bayesian combined mtDNA tree (Figure 41) in the discussion of the taxonomic status of *T. mauritanica* in North Africa for these reasons:

1- The Bayesian combined cladogram was built based on 1433 bp mtDNA sequences.

2- The statistical support of this tree is very high, the Bayesian posterior probability values were high, and such high values are considered to be good indicators of robustness of branches.

3- The evolutionary histories of the major lineages were revealed.

There is an urgent need for taxonomic revision for *T. mauritanica* in North Africa; the genetically and morphologically studied *Tarentola* in this region (south-central Tunisia, Libya, and Egypt) should be assigned to *T. fascicularis* (a former subspecies of *T. mauritanica*), except clade B and F (*T. neglecta*, *T. mindiae*, and *T. deserti*) which clearly constitute separate species from *T. fascicularis* (Joger and Bshaena, 2010). Elevation of *fascicularis* to species rank is largely concordant with data of Joger (2003), who explains the presence of a mixture of morphological features uniting all of north-west Libyan population of *Tarentola* with population of south Tunisian (Djerba island), according to these characters we could assign these populations to *T. mauritanica*, but electrophoetically these populations seem to be closer to *T. deserti*, however, in the same time Joger stressed the importance of *T. (m).fascicularis* from Libya and Egypt in such a

decision, ‘‘they should be taken into account’’. Also this elevation is concordant with data of Harris et al. (2009) and Rato et al. (2010), who distinguished two basal divisions in the subgenus *Tarentola*. One of these branches leads to *T. deserti and T. boehmei* from Morocco, another to *T. angustimentalis* from Canary Islands and *T. mauritanica* from south Europe, Morocco, Algeria and northern Tunisia on one side and to *T. m. fascicularis* from Libya and *Tarentola* from Italian Islands (Lampedusa Island and Conigli Islet) on the other side. Single individuals of ‘‘*T. mauritanica*” from Algeria and of “*T. deserti*” from Morocco, both were loosely connected to the latter clade, but we do not know which taxa were actually represented by those samples. The Tunisian samples used by these authors clustered with *T. m. mauritanica*, but they were exclusively from northwestern Tunisia.

From the results obtained (from both morphological and molecular phylogenetic study), and as discussed above, we confirm the presence of these taxa:

1- The presence of *T. deserti* in NW-Libya was recorded, and this is keeping with one of the assumptions in this study. The NW-Libyan *deserti* is almost identical with NW-African *deserti* in our mtDNA analyses. However, because of the existence of significant differences at least in some morphological characters between NW-African *deserti* and NW- Libyan group, the Libyan group should be introduced as separated subspecies of *T. deserti* (*T. deserti* ssp. nov.)

2- Previous studies (Schleich et al, 1996) proposing the existence of *T. neglecta* in northwestern Libya (Tripolitania). But, in spite of intensive field work in this region, we have not been able to prove that. However, the presence of *T. neglecta* in southwestern Libyan Oases was recorded, and this is consistent with one of the assumptions in this study. Although the SW-Libyan samples of *neglecta* are almost identical with the Algerian specimens in our mtDNA analyses, they differ in morphological characters. There are significant differences at least in some morphological features between each of SW-Libyan *neglecta*,

northern Sahara *T. n. neglecta* and central Sahara *T. n. geyri*. The Libyan populations are geographically isolated (about 600 km) from both known subspecies of *T. neglecta*. As is well known, the dramatic changes of Holocene pluvial lead to the desertification of the North African Sahara. Nine thousand years ago the Sahara desert was a green savannah (Gasse et al, 1990). Today, the desertification limits the existence of the Libyan population of *T. neglecta* to the south-west Libyan Sahara Oases, which might be old relict populations from a time when this species was abundant all over North Africa Sahara, and in direct contact with the *neglecta* population of Algeria. Therefore Libyan group should be assigned to a new subspecies of *neglecta* (*T. neglecta* ssp. nov.).

3- Our results confirm the presence of *T. f. fascicularis* (former subspecies *T. (m). fascicularis*) in only Aljabal Alakhdar area (northeastern Libya); and not, as previously thought (Joger, 1984; Schleich et al, 1996), in a narrow band along the Mediterranean coast across northern Libya.

4- A new subspecies of *T. fascicularis* endemic to north-east Libya (Cyrenaica), known from Ras Lanuf and Marsa El Prega was recorded. In all our mtDNA analyses this group (*T. fascicularis* ssp. nov.) separates as a monophyletic clade. Also these geckos possess significant morphological characters which distinguish them from all other groups in the morphological analyses.

5- A new subspecies of *T. fascicularis* endemic to Cyrenaica (Aljabal Alakhdar area: namely known from Taknis), this new subspecies (*T. fascicularis* ssp. nov.) resolved as sister clade to group Ras Lanuf and Marsa El Prega in mtDNA analyses. However, the morphological study of Taknis group showed, this group possess at least some significant morphological characters which distinguish them from all other groups in the analysis.

6- A new subspecies of *T. fascicularis* endemic to south-west Libyan Sahara desert, known from Sabha province. This group is distinguished from all other groups in mtDNA analyses; as well as in morphological analyses, they differ significantly from all other groups, and separate in DFA and PCA plots.

7- A new taxon endemic to north-central Libya (Suirt basin) detected as new subspecies of *T. fascicularis*. This group (based on mtDNA data) forms a sister lineage to Sabha *T. fascicularis* ssp. nov.; as well as in the morphological study, this group possesses significant morphological features which distinguish them from all other groups in the analysis.

8- A new subspecies of *T. fascicularis* distributed in northwestern Libya (Tripolitania), and also in southwestern Libya (namely: Tcarkiba and El Perkat). This group (based on mtDNA data) forms a robust monophyletic assemblage. In morphological analysis, this group possesses significant morphological features which distinguish them from all other groups, and all individuals from this distribution range cluster together in (PCA and DFA plots).

9- A new subspecies of *T. fascicularis* endemic to Central Tunisia (namely: known from Djebel Orbata-Gafsa), this new subspecies *T. fascicularis wolfgangi* ssp.nov. Joger and Bshaena (2010) forms a monophyletic lineage in all individual and combined mtDNA analyses; in morphological analysis, this group possesses significant morphological features which distinguish them from all other groups in the analysis.

Through the results reached from both morphological and molecular phylogenetic studies, we reject the following hypotheses:

1- The existence of *T. mindiae* in northern Cyrenaica. Through our field work, and the intensive sampling in northeastern Libya (Cyrenaica), we did not record any sample of this species (*T. mindiae*) in this region. And therefore we reject the point of view that, many inland records of *T.*

mauritanica in Cyrenaica refer to *T. mindiae* (Baha El Din, 2006). However, depending on our results, most or all specimens who were collected from this region (Cyrenaica) assigned to different new subspecies of *T. fascicularis.*

2- The existence of the new subspecies from south-central Tunisia *T. fascicularis wolfgangi* in north-west Libya (Tripolitania), though this subspecies is closely related phylogenetically to northwestern Libyan population of *T. fascicularis* ssp. nov., as well as morphologically. Despite our intensive sampling in Tripolitania we did not record the existence of the south-central Tunisian subspecies in northwestern Libya.

3- The existence of *T. m. mauritanica* in Libya. Although quite a number of previous studies in Libya (Zavattari, 1930; Frynta et al, 2000; Ibrahim, 2008) report the existence of this species in Libya, however, in spite of intensive field research, we could not get even one specimen of this species from any site in Libya. Thus, we could not confirm the existence of this species in Libya.

4.6. Taxonomic conclusions

In this section we provide a description of the new taxa.

1*. Tarentola* (*Tarentola*) *deserti* ssp. nov.-Libya

Holotype: SNHM-BS 40114 (Staatliches Naturhistorisches Museum, Braunschweig), an adult male, collected by Ismail M.Bshaena on 17.05.2007 (Figure 50).

Terra typica: Itwellia (Tripolitania, N: 32° 34' 07.64'', E: 11° 59' 02.89'', 57 m above sea level, north-west Libya), from ruins of abandoned buildings.

Paratypes: (n=64) SNHM-BS 40000, 40002-3, 40005-6, 40009 from Rass Elifa; SHNM-BS 39945-46, 39948, 39950, 39952-57, 39997 from El Sahla; SNHM-BS 40102-5, 40107-13, 40115-25 from Itwellia; SNHM-BS 40127, 40129 from Misratah; SNHM-BS 40079-101 from Azzawiah.

Distribution: Common and widespread in northwest regions of Libya (Tripolitania), from Azzawiah and seen to extend further west to Libyan-Tunisian borders, and extends to a depth of 70 km to the south (Figure 60). It is also observed in Misratah (about 255 km to the east of Azzawiah). It is mainly nocturnal and found in or near human habitation, close to artificial lights at night where it captures insects, it is also collected from ruins of abandoned buildings, walls, slots, under bridges, and from trees under crust.

Diagnosis: *Tarentola deserti* ssp. nov has a medium size: maximum SVL= 77.72 mm versus 80.32 mm in *T. d. deserti* from northwestern Africa. The number of dorsal tubercles in the axilla-groin distance (12-14, versus 12-15 in *T. d. deserti* from northwestern Africa) in the same distance; dorsal tubercles giving place to ventral scales without a definite zone of transitional scales; tendency for a lower number of subdigital lamellae under the first toe with only a slight overlap (10-11, versus 11-14 in *T. d. deserti* from northwestern Africa); lower number of subdigital lamellae under the fourth toe (15-17 versus 16-19 in *T. d. deserti* from northwestern Africa); lower number of subdigital lamellae under the fifth toe with only a slight overlap (19-22, versus 21-24 in *T. d. deserti* from northwestern

Africa). Regarding coloration, there is variation in the color, adult individuals have whitish gray, light pink, or beige to reddish dark brown color, with pattern of 4-5 transversal bars which are often reduced to patches or lack altogether; Iris yellowish-ochre. The new subspecies shares with northwestern African *T. d. deserti* the condition of dorsal tubercles transitioning to ventral scales without a conspicuous zone of granules; however, the Libyan subspecies, beside been smaller in size, differs from *T. deserti* North Africa by having a higher number of dorsal tubercles (12-14) versus (12-13) in North African *T. deserti* . Also differs in the range number of ventral scales, 38-43 versus 33-39 in the *T. deserti* ssp. nov from northwestern Africa; and differs in the range number of gular scales, 40-51 versus 45-63 in North African *T. deserti*.

Description: Size small [maximum SVL: 77.72]; maximum head length 24.87 mm (head length 31–32% of SVL); head width 9.92-18.92 mm (x=14.42, n=69, head width 71-79% of head length);head height 5.5-11,9mm (x=8.70, n=69, head height 40-49% of head length); eye diameter 2.80-3.99 mm (x=3.39, n=69, 16-20% of head length); tail length 1.1–1.2 times longer than body.

Figure 50. Holotype of *Tarentola deserti* ssp. nov. Itwellia, Tripolitania, north-west Libya

Dorsum covered by slightly pointed, enlarged keeled tubercles arranged in 12-14 (mode 13, n=69) transversal rows at midbody; ventral scales smooth, forming 38-43 (mode 40, n=69) rows at midbody; interorbital scales 14-16 (mode 15, n=69); rostral in contact with nostril; first toe lamellae 8–12 (n=69).

Description of the Holotype: Robustly built lizard, snout-vent length: 77.72 mm; tail length: 61.23 mm (regenerated tip); head length: 24.06 mm; head width: 18.98 mm; head height: 11.91 mm; eye diameter: 3.99 mm; ASL (distance from the front edge of eye up to snout tip): 7.56 mm; AOL (distance from the posterior edge of the eye to the ear opening):7.74 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:15.38 mm; IOB (interorbital distance): 10.24 mm; FLL: 28.64 mm; HLL: 35.1 mm; HDL: 6.48 mm; HDW: 3.5 mm; FHLL: 38.68 mm; sublabial scales: 8; supralabial scales: 8; IOA (interorbital scales): 15; dorsal tubercles in the axilla-groin distance: 14; ventral scales in the axilla-groin distance: 42; 12 lamellae underneath of the first toe ; 16 lamellae underneath of the fourth toe; 22 lamellae underneath of the fifth toe; 50 gular scales from mental scale to gular fold; Cr: 6; dorsal tubercles are, pyramidal, sharply, central keeled, encircled by a row of secondary tubercles, rosettes of 7 medium-size scales in a horse shoe-like formation; tubercles are separated laterally from each other by 2-3 small scales; there are 3 scales that are somehow bigger than the gular scales in contact with mental; coloration: reddish (dark brown), with 5 dark brown cross bars ; iris: yellowish ochre.

2. *Tarentola* (*Tarentola*) *fascicularis fascicularis* -Libya

SNHM-BS 40137 (Staatliches Naturhistorisches Museum, Braunschweig), an adult female, collected by Ismail M.Bshaena on 22.05.2007 (Figure 51).

Terra typica: Tobruk (Cyrenaica, N: 32° 02’ 34.17’’- E: 23° 57’ 48.26’’, 83 m above sea level, north-east Libya), from firm ground, near artificial lights at night.

Paratypes: (n=14) SNHM-BS40131-32 from Desert road between Ajdabiya &Tobruk, SNHM-BS40134-36 from Tobruk, and SHNM-BS40153-61 from Sidi Massod.

Distribution: In Libya, it is common and widespread in the north-east regions (Cyrenaica), and 180 km into the south from the Mediterranean coast (Figure 62), it is found in desert road Ajdabiya-Tobruk and extended eastward to Tobruk in the extreme east Libya, it is also observed in Green Mountain in Sidi Massod. In desert road Ajdabiya-Tobruk and Tobruk, the animals were collected from dry stone desert areas, under rocks, and also from abandoned ruins buildings; in Sidi Massod the animals were collected from trees, under rocks, and also from honey-bees boxes (this could be evidence or support of Feeding of honey or nectar). In Egypt, it is found in northern portion of the country along Mediterranean coast (Baha El Din, 2006).

Diagnosis: *Tarentola fascicularis fascicularis* has a medium size: maximum SVL= 65.19 mm versus 84 mm in *T. f. fascicularis* Egypt (former *T. m. fascicularis*). Dorsal tubercles are multi-keeled, and surround by rosettes of 5-8 medium-sized scales, but tubercles are separated laterally from each other by 1-3 medium-sized scales in *T. f. fascicularis* Libya versus 4-5 small-sized scales in *T. f. fascicularis* Egypt. On the border between dorsal and ventral tubercles interspersed with large scales; tendency for a higher number of subdigital lamellae under fifth toe, there is an average of 19 lamellae versus 17 in *T. f. fascicularis* Egypt (Joger, 1984; Baha El Din, 2006). Regarding coloration, there are divergences in the color, adult individuals from Tobruk, desert road Ajddabiya-Tobruk, Um Arrizam, and Egypt have whitish gray or light-yellowish color, with pattern of 4-5 light-brown transversal bars, sometimes indistinct transverse bands; while individuals from Sidi Massod have medium-brown color, with pattern of 4-5 dark transversal bars. On the other hand, the Libyan *T. f. fascicularis,* beside have a higher number of dorsal tubercles 10-16 versus 13-14 in *T. fascicularis* ssp. nov.- sister group Ras Lanuf, differs from *T. fascicularis* ssp. nov.- sister group Ras Lanuf in the pattern of dorsal tubercles, *T. f. fascicularis* covered by enlarged multi-keeled tubercles versus oval-shaped,

simple-keeled tubercles in *T. fascicularis* ssp. nov.- sister group Ras Lanuf; also they have a lower number of lamellae underneath the first toe 9-10, versus 10-11 in the *T. fascicularis* ssp. nov.- sister Ras Lanuf.

Figure 51. *Tarentola fascicularis fascicularis*, Tobruk (extreme northeastern Libya).

Description: medium-sized [SVL: 42.79-65.19 (x=53.99, n=15)]; head length 13.56-20.36 mm (x=16.96, n=15, head length 31-32% of SVL); head width 9.6-15.4 mm (x=12.5, n=15, head width 71-76% of head length);head Height 5.34-9.14 mm (x=7.24, n=15, head height 39-45% of head length); eye diameter 3.09-4.09 mm (x=3.59, n=15, 20-23% of head length); gular scales 38-46 (15). Dorsum covered by enlarged multi-keeled tubercles arranged in 10-16 (n=15) transversal rows at midbody; ventral scales smooth, forming 33-40 (mode 36, n=15) rows at midbody; interorbital scales 13-15 (mode 14, n=15); first toe lamellae 9-10 (n=15), fourth toe lamellae 13-16 (n=15); fifth toe lamellae 18-21 (n=15).

Description of the Holotype: Snout-vent length: 64.79 mm; tail length: 73.56 mm; head length: 18.21 mm; head width: 14.55 mm; head height: 9.07 mm; eye

diameter: 3.34 mm; ASL (distance from the front edge of eye up to snout tip): 6.56 mm; AOL (distance from the posterior edge of the eye to the ear opening):6.05 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:12.46 mm; IOB (interorbital distance): 7.88 mm; FLL: 20.89 mm; HLL: 26.57 mm; HDL: 5.37 mm; HDW: 2.37 mm; FHLL: 32.38 mm; sublabial scales: 8; supralabial scales: 8; IOA (interorbital scales): 15; dorsal tubercles in the axilla-groin distance: 14; ventral scales in the axilla-groin distance: 38; 9 lamellae underneath of the first toe ; 15 lamellae underneath of the fourth toe; 20 lamellae underneath of the fifth toe; 44 gular scales from mental scale to gular fold; there is 2 scales that are big in size in contact with mental; Cr: 5; dorsal tubercles are, oval-shape, multi-keeled with black spots, surrounded by a row of secondary tubercles, rosettes of 7 medium-sized scales (horseshoe-shaped). tubercles are separated laterally from each other by 1-2 medium-sized scales; coloration: color of dorsum light-yellow, with 4 light-brown cross bars, which extend on to tail as lines (12 dark brown lines), ventral side is white with scattered black spots.

3. *Tarentola* (*Tarentola*) *fascicularis* ssp. nov.-Ras Lanuf

Holotype: SNHM-BS 40140 (Staatliches Naturhistorisches Museum, Braunschweig), an adult male, collected by Ismail M.Bshaena on 24.05.2007 (Figure 52).

Terra typica: Ras Lanuf (Cyrenaica, N: 30° 29’ 56.12’’- E: 18° 31’ 26.01’’, 13 m above sea level, north-east Libya), from ruins of abandoned buildings.

Paratypes: (n=9). SNHM-BS 40138-39, 40141-42, 40189 from Ras Lanuf; SNHM-BS 40131 from desert road Ajdabiya-Tobruk; and SNHM-BS 40143-45 from Marsa El Brega.

Distribution: Restricted to Ras Lanuf, Marsa El Brega, and desert road Ajdabiya-Tobruk, it is has been found in dry areas (arid areas, with sandy desert

and little vegetation, in old buildings cracks and on trees). In Ras Lanuf and Marsa El Brega the geckos were observed close to sea coast.

Diagnosis: *Tarentola fascicularis* ssp. nov has a big size: maximum SVL= 96.36 mm versus 80.32 mm in *T. d. deserti* NW- Africa, 77.72 mm in *T. deserti* ssp. nov -Libya, 65.19 mm, 64.40 mm in *T. f. fascicularis* northeastern Libya and *T. fascicularis* ssp. nov.-sister group Ras Lanuf respectively. They have (more or less) the same number of dorsal tubercles in the axilla-groin distance (13-14, versus 12-14 in both *T. deserti* NW- Africa and *T. deserti* ssp. nov Libya) in the same distance; dorsal tubercles giving place to ventral scales without a definite zone of transitional scales; tendency for a lower number of subdigital lamellae under the first toe with only a slight overlap (11-12, versus 11-14 in *T. deserti* northwestern Africa); lower number of subdigital lamellae under the fourth toe (15-18 versus 16-19 *T. deserti* northwestern Africa); the number of subdigital lamellae under the fifth toe with only a slight overlap (19-24, versus 21-24 in *T. deserti* northwestern Africa); while *T. deserti* ssp. nov.- Libya, *T. fascicularis* ssp. nov.- sister group Ras Lanuf, and *T. f. fascicularis* northeastern-Libya have low number of subdigital lamellae under the fifth toe (19-22, 19-22, 18-21 respectively). Regarding coloration, adult individuals have whitish gray or light gray-brown color, with pattern of 4-5 transversal bars. Iris yellowish-ochre. The new subspecies of *T. fascicularis* shares with *T. deserti* the condition of dorsal tubercles transitioning to ventral scales without a conspicuous zone of granules; however, the new subspecies, beside being larger in size, differs from NW-Africa *T. deserti* in the color patterns, the color of new subspecies was as described above, while in *T. deserti* was arranged from light pink to orange, sometimes beige to reddish or dark brown, and in most cases with reduced or without transversal bars. They have (more or less) the same number of interorbital scales (12-16 versus 14-16 in *T. deseri* ssp. nov.- Libya), and It is differs from NW-African *T. deserti*, *T. fascicularis* ssp. nov.- sister group Ras Lanuf and *T. f. fascicularis* Libya which have lower number of interorbital scales (13-15); They have (more or less) the same number of gular scales (27-51 versus 40-51 in *T. deserti* ssp. nov.- Libya), It is differs from *T. fascicularis* ssp. nov.- sister

group Ras Lanuf and Libyan *T. f. fascicularis* which have lower number of gular scales (it were 40-47, 38-46 respectively), and also differs from NW-African *T. deserti* which has a higher number of gular scales (it was 45-63)*;* The new subspecies have higher number of ventral scales which (more or less) the same number (37-42 versus 38-43 in Libyan *T. deserti* ssp. nov.), and differs from *T. fascicularis* ssp. nov.-sister group Ras Lanuf, *T. f. fascicularis* Libya, and NW-African *T. deserti* which have lower number of ventral scales, (it was 35-38, 33-40 and 33-39 respectively)*.*

Description: Robustly built lizard, big-sized [maximum SVL: 96.4]; with big boarder head, head length up to 28 mm (head length 29-32% of SVL); head width up to 22.96 mm (head width 76-82% of head length);head Height up to 13.61 mm (head height 44-49% of head length); eye diameter 3.79-5,19 mm (x=4.49, n=6, 18-24% of head length); rostral in contact with nostril. Dorsum covered with regular bands of sharply protruding enlarged keeled tubercles, arranged in 13-14 (n=6) transversal rows at midbody; ventral scales smooth, forming 38-42 (mode 40, n=6) rows at midbody; interorbital scales 13-16 (mode 15, n=6); first toe lamellae 11-12(n=6).

Figure 52. Holotype of *Tarentola fascicularis* ssp. nov.- Ras Lanuf, Cyrenaica-Libya

Description of the Holotype: Snout-vent length: 96.36 mm; tail length: 92.36 mm; head length: 28.00 mm; head width: 22.68 mm; head height: 13.52 mm; eye diameter: 5.2 mm; ASL (distance from the front edge of eye up to snout tip): 10.05 mm; AOL (distance from the posterior edge of the eye to the ear opening):10.12 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:18.80 mm; IOB (interorbital distance): 12.71 mm; FLL: 33.59 mm; HLL: 45.75 mm; HDL: 9.28 mm; HDW: 3.04 mm; FHLL: 45.26 mm; sublabial scales: 9; supralabial scales: 8; IOA (interorbital scales): 16; dorsal tubercles in the axilla-groin distance: 14; ventral scales in the axilla-groin distance: 40; BT: 120; 12 lamellae underneath of the first toe ; 18 lamellae underneath of the fourth toe; 23 lamellae underneath of the fifth toe; 53 gular scales from mental scale to gular fold; there is 4 scales that are somehow from the same size as gular scales in contact with mental Cr: 6; dorsal tubercles are, pyramidal, strong central keeled with black spots, surrounded by a row of secondary tubercles, rosettes of 8 medium-size keeled scales. tubercles are separated laterally from each other by 3-4 small-size scales; coloration: color of dorsum light gray or gray-brown, with 5 dark brown cross bars, which extend on to tail as lines (9 dark brown lines), ventral side is white; iris: yellowish ochre.

4. *Tarentola* (*Tarentola*) *fascicularis* ssp. nov. – (sister group Ras Lanuf Libya)

Holotype: SNHM-BS 40176 (Staatliches Naturhistorisches Museum, Braunschweig), an adult male, collected by Ismail M.Bshaena on 05.07.2007 (Figure 53).

Terra typica: Ajdabiya (Cyrenaica, N: 30° 44’ 20.02’’- E: 20° 12’ 27.04’’, 0 m above sea level, north-east Libya), from *Acacia* tree under crust in sandy area.

Paratypes: (n=13) SNHM-BS40173-74 from Ajdabiya; SNHM-BS40162-65 from Benghazi; and SNHM-BS40166-72 from Taknis.

Distribution: new taxon observed in Cyrenaica (north-east Libya), specimens were collected from Ajdabiya and Banghazi from arid areas with little vegetation (Figure 65); the geckos were captured from *Acacia* trees, also from scattered broken dry branches under crust; the animals also found in Green mountain in Taknis, in this region lizards were found inside a forest of *Acacia* trees.

Figure 53. Holotype of *Tarentola fascicularis* ssp. nov.- Ajdabiya (Cyrenaica) northeastern Libya

Diagnosis: *Tarentola fascicularis* ssp. nov has a medium size: maximum SVL= 64.40 mm versus 96.36 mm in *T. fascicularis* ssp. nov. - Ras Lanuf. A tendency towards the same range of dorsal tubercles in the axilla-groin distance (13-14) in the same distance; dorsal tubercles giving place to ventral scales without a definite zone of transitional scales; tendency for a lower number of subdigital lamellae in the first toe with only a slight overlap (10-11, versus 11-12 in *T. fascicularis* ssp. nov.- Ras Lanuf); about the same number of subdigital lamellae in the fourth toe with overlap (14-18 versus 15-18 in *T. fascicularis* ssp. nov.- Ras Lanuf); tendency for a lower number of subdigital lamellae in the fifth toe with only a slight overlap (19-22, versus 19-24 in *T. fascicularis* ssp. nov.- Ras Lanuf). Regarding coloration, adult individuals have light-brown color, with pattern of 5 dark cross bars on the dorsal side, these cross bars extends from the

neck to sacral region, and extend on to tail as cross-sectional lines (10-14 dark lines). The new subspecies shares with *T. fascicularis* ssp. nov.- Ras Lanuf the condition of dorsal tubercles transitioning to ventral scales without a conspicuous zone of granules; however, the new subspecies, beside been smaller in size, differs from *T. fascicularis* ssp. nov.- Ras Lanuf in the pattern of dorsal tubercles, the dorsal tubercles of new species is, oval-shaped, simple keeled and non-sharp; while in *T. fascicularis* ssp. nov.- Ras Lanuf was pyramidal, strong central keeled, also differ in the number of gular scales, the new subspecies have 40-47 versus 37-51 in *T. fascicularis* ssp. nov.- Ras Lanuf. It is also differs in the number of ventral scales, it was 35-38 versus 37-42 in *T. fascicularis* ssp. nov. - Ras Lanuf.

Description: medium size [SVL: 40.60-64.40 (x=52.50, n=13)]; head length 13.31-19.71 mm (x=16.51, n=13, head length 31-33% of SVL); head width 9.53-14.93 mm (x=12.23, n=13, head width 72-76% of head length); head Height 5.30-9.80 mm (x=7.10, n=13, head height 40-45% of head length); eye diameter 2.72-4.12 mm (x=3.42, n=13, eye diameter 20-21% of head length). Dorsum covered by enlarged oval-shaped, simply keeled, non-sharp tubercles arranged in 13-14 (n=13) transversal rows at midbody; ventral scales smooth, forming 35-38 (n=13) rows at midbody; interorbital scales 13-15 (n=13); 10-11 lamellae underneath of the first toe (n=13); 14-18 lamellae underneath of the fourth toe (n=3); and 19-22 lamellae underneath of the fifth toe (n=13).

Description of the Holotype: Snout-vent length: 62.35mm; tail length: 72.90 ; head length: 18.9 mm; head width: 14.04 mm; head height: 8.25 mm; eye diameter: 3.7 mm; ASL (distance from the front edge of eye up to snout tip): 6.07 mm; AOL (distance from the posterior edge of the eye to the ear opening): 5.22 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:12.43 mm; IOB (interorbital distance): 8.05 mm; FLL: 25.36 mm; HLL: 29.75 mm; HDL: 5.59 mm; HDW: 2.55 mm; FHLL: 31.28 mm; sublabial scales: 8; supralabial scales: 9; IOA (interorbital scales): 12; rostral in contact with nostril; dorsal tubercles in the axilla-groin distance: 13; ventral

scales in the axilla-groin distance: 36; 11 lamellae underneath of the first toe ; 16 lamellae underneath of the fourth toe; 22 lamellae underneath of the fifth toe; 41 gular scales from mental scale to gular fold; there is 2 scales that are somehow big in size as gular scales in contact with mental Cr: 5. Dorsal tubercles are: oval-shaped, simple, central keeled, non-acute, and surrounded by a row of secondary tubercles 7-6, dorsal tubercles are separated laterally from each other by 1-3 medium-size scales. Coloration: color of dorsum light-brown, with 5 dark-brown cross bars on the dorsal side, these cross bars extends from the neck to sacral region, and extend on to tail as cross-sectional lines(14 dark-brown lines), ventral side is white with scattered small black spots.

5. *Tarentola* (*Tarentola*) *fascicularis* ssp. nov.–Sabha

Holotype: ZCMV 10706, an adult male, collected by Ismail M.Bshaena in October 2008 (Figure 54).

Terra typica: Sabha (South Libyan Sahara desert, N: 27° 00' 04.10''- E: 14° 28' 37.37'', 427 m above sea level, south-west Libya), from a stable of cattle.

Paratypes: (n=7) ZCMV10701, 10703-4, 10707-8, 10710, and 10713 from Sabha.

Distribution: The gecko seemed to be widespread and common in Sabha, observed in dry stone-desert under rocks, in old buildings, from scattered trees and shrubs; it was also captured from human settlements. This gecko has been described as *T.mauritanica* (Moorish gecko) by Ibrahim, 2008.

Diagnosis: *Tarentola fascicularis* ssp. nov. Sabha has a big size: maximum SVL= 73.76 mm versus 68.00 mm in *T. fascicularis* ssp. nov. - Suirt (sister group Sabha). A tendency towards a higher number of scales rows around the midbody (13-15, versus 12-14 in *T. fascicularis* ssp. nov.- Suirt) in the same distance; dorsal tubercles giving place to ventral scales without a definite zone of transitional scales; tendency for a higher number of subdigital lamellae in the first

toe with only a slight overlap (12-14, versus 11-12 in *T. fascicularis* ssp. nov.- Suirt); a higher number of subdigital lamellae in the fourth toe with overlap (17-19 versus 16-18 in *T. fascicularis* ssp. nov.- Suirt); tendency for a same number of subdigital lamellae in the fifth toe (21-23, versus 21-23 in *T. fascicularis* ssp. nov.- Suirt). Regarding coloration, adult individuals have light brown color, with pattern of pale- brown cross bars run on the dorsal region. The new subspecies shares with *T. fascicularis* ssp. nov.- Suirt the condition of dorsal tubercles transitioning to ventral scales without a conspicuous zone of granules, also the condition of nostril (rostral in contact with nostril); however, the new subspecies, beside been larger in size, differs from *T. fascicularis* ssp. nov.- Suirt in the pattern of dorsal tubercles, the new subspecies covered by semi-round shaped, simple central keeled enlarged tubercles, and arranged in 13-15 transversal rows at midbody; while in *T. fascicularis* ssp. nov.- Suirt covered by sharp-pyramidal shape, central keeled enlarged tubercles, which arranged in 12-14 transversal rows at midbody. It is also differs in the range number of ventral scales, it was 40-43 in new subspecies versus 35-41 in *T. fascicularis* ssp. nov.- Suirt; and also the number of gular scales, it was arranged in 44-51 in new subspecies versus 48-52 in *T. fascicularis* ssp. nov.- Suirt.

Figure 54. Holotype of *Tarentola fascicularis* ssp. nov.- Sabha, southwestern Libyan Sahara desert

Description: medium size [SVL: 37.56-73.76 (x=55.66, n=8)]; head length 12.6-21.6 mm (x=17.1, n=8, head length 29-33% of SVL); head width 8.6-16.8 mm (x=12.7, n=8 head width 68-78% of head length); head Height 5.14-10.34 mm (x=7.74, n=8, head height 41-48% of head length); eye diameter 3.04-4.64 mm (x=3.84, n=8, eye diameter 21-24% of head length). Dorsum covered by enlarged semi-round, simple keeled tubercles arranged in 13-15 (mode 14, n=8) transversal rows at midbody; ventral scales smooth, forming 40-43 (n=8) rows at midbody; interorbital scales 14-15 (n=13); 12-14 lamellae underneath of the first toe (n=8); 17-19 lamellae underneath of the fourth toe (n=8); 21-23 lamellae underneath of the fifth toe (n=8).

Description of the Holotype: Snout-vent length: 66.62 mm; tail: 79.02; head length: 19.84 mm; head width: 15.07 mm; head height: 8.97 mm; eye diameter: 4.31 mm; ASL (distance from the front edge of eye up to snout tip): 7.16 mm; AOL (distance from the posterior edge of the eye to the ear opening): 5.81 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:17.42 mm; IOB (interorbital distance): 8.51 mm; rostral in contact with nostril; FLL: 25.41 mm; HLL: 33.48 mm; HDL: 7.58 mm; HDW: 2.85 mm; FHLL: 33.28 mm; sublabial scales: 8; supralabial scales: 10; IOA (interorbital scales): 15; dorsal tubercles in the axilla-groin distance: 15; ventral scales in the axilla-groin distance: 42; BT: 174; 14 lamellae underneath of the first toe ; 19 lamellae underneath of the fourth toe; 23 lamellae underneath of the fifth toe; 50 gular scales from mental scale to gular fold; there is 3 scales that are somehow from the same size as gular scales in contact with mental Cr: 5. Dorsal tubercles are: tend to found in shape or semi-round, simple, central keeled, and surrounded by a row of 7-10 secondary tubercles (rosettes) of medium size, dorsal tubercles are separated laterally from each other by 3-4 small-size scales. Coloration: basic color of dorsum light-brown or beige, with five pale-brown cross bars on the dorsal side, these cross bars extends from the neck to sacral region, and extend on to tail as cross-sectional lines (8 pale-brown lines), and ventral side is white.

6. *Tarentola* (*Tarentola*) *fascicularis* ssp. nov.–Suirt (sister group Sabha)

Holotype: SNHM-BS 40148 (Staatliches Naturhistorisches Museum, Braunschweig), an adult female, collected by Ismail M.Bshaena on 25.05.2007 (Figure 55).

Terra typica: Suirt (Cyrenaica, N: 31° 10' 53.72''- E: 16° 45' 46.85'', 29 m above sea level, north-central Libya), from tree under crust.

Paratypes: (n=3) SNHM-BS40146-47, 40149 from Suirt.

Distribution: So far common and widespread in the north-central region of Libya (Suirt), at low elevations, it does not seem to extend further east. It has been collected from dry-stone area with scattered trees and shrubs, the animals were captured from *Acacia* trees, also from broken-dry branches, and under rocks.

Diagnosis: *T. fascicularis* ssp. nov.-Suirt has a medium size: maximum SVL= 68.00 mm versus 73.76 mm in *T. fascicularis* ssp. nov. - Sabha. A tendency towards a lower number of dorsal tubercles in the axilla-groin distance despite a

Figure 55. Holotype of *Tarentola fascicularis* ssp. nov.-Suirt, north-central Libya

slight overlap (12-14, versus 13-15 in *T. fascicularis* ssp. nov.- Sabha) in the same distance; dorsal tubercles giving place to ventral scales without a definite zone of transitional scales (as present in *T. fascicularis* ssp. nov.- Sabha); tendency for a lower number of subdigital lamellae in the first toe with only a slight overlap (11-12, versus 12-14 in *T. fascicularis* ssp. nov.- Sabha); lower number of subdigital lamellae in the fourth toe with only a slight overlap (16-18 versus 17-19 in *T. fascicularis* ssp. nov.- Sabha); the same number of subdigital lamellae in the fifth toe with (21-23, versus 21-23 in *T. fascicularis* ssp. nov.- Sabha). Regarding coloration, adult individuals have light-brown to light-reddish color, with pattern of 4-5 dark transversal bars or x-shape. Several dark lines run on the snout from the rostral through the eye some time forms Y-shapes. The new subspecies shares with South Libyan *T. fascicularis* ssp. nov.- Sabha the condition of dorsal tubercles transitioning to ventral scales without a conspicuous zone of granules; nevertheless, the new subspecies, beside been smaller in size, differs from *T. fascicularis* ssp. nov.- Sabha by having a lower number of ventral scales 35-41 (mode: 38), versus 40-43 (mode: 41); and a higher number of gular scales 48-52 (mode: 50) versus 44-51 (mode: 47) in *T. fascicularis* ssp. nov.- Sabha.

Description: size medium [SVL: 54.46-68.00 (x=61.23, n=4)]; head length 16.01-21.61 mm (x=18.81, n=4, head length 29-32% of SVL); head width 11.99-15.99 mm (x=13.99, n=4, head width 74-75% of head length); head Height 6.52-9.72 mm (x=8.12, n=4, head height 41-45% of head length); eye diameter 3.27-4.47 mm (x=3.87, n=4, eye diameter 20-21% of head length). Dorsum covered by enlarged tubercles, which have sharp-pyramidal shape, central keeled, and arranged in 12-14 (n=4) transversal rows at midbody; ventral scales smooth, medium in size, forming 35-41(n=4) rows at midbody; interorbital scales 13-15 (n=4); rostral in contact with nostril; 11-12 lamellae underneath of the first toe (n=4); 16-18 lamellae underneath of the fourth toe (n=4); and 21-23 lamellae underneath of the fifth toe (n=4).

Description of the Holotype: Snout-vent length: 68.00 mm; tail length: 79.02 ; head length: 21.03 mm; head width: 15.36 mm; head height: 9.53 mm; eye

diameter: 4.49 mm; ASL (distance from the front edge of eye up to snout tip): 7.16 mm; AOL (distance from the posterior edge of the eye to the ear opening): 6.03 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:12.88 mm; IOB (interorbital distance): 7.87 mm; FLL: 25.00 mm; HLL: 31.7 mm; HDL: 4.94 mm; HDW: 2.38 mm; FHLL: 30.25 mm; sublabial scales: 8; supralabial scales: 8; IOA (interorbital scales): 15; dorsal tubercles in the axilla-groin distance: 14; ventral scales in the axilla-groin distance: 37; BT: 120; 11 lamellae underneath of the first toe ; 18 lamellae underneath of the fourth toe; 22 lamellae underneath of the fifth toe; 52 gular scales from mental scale to gular fold; there is 3 scales that are somehow from the same size as gular scales in contact with mental Cr: 7. Dorsal tubercles are: with sharp-pyramidal shape, central keeled with black spots, encircled by a row of secondary tubercles, rosettes of 8 big-size scales in a horse shoe-like formation; tubercles are separated laterally from each other by 3 small scales. There is 3 scales that are in direct contact with mental, it is from the same size of the gular scales. Coloration: basic color of dorsum light-brown, with pattern of 4 dark cross bars (or x-shape), run on the dorsal side from neck to sacral region, on the head dark lines or streaks deployed in a non regular directions, form Y-shape on the snout, tail with 12 lateral dark lines; ventral side is white.

7. *Tarentola* (*Tarentola*) *fascicularis* ssp. nov. - complex Libya

Holotype: SNHM-BS40078 (Staatliches Naturhistorisches Museum, Braunschweig), an adult male, collected by Ismail M.Bshaena on 16.05.2007 (Figure 56).

Terra typica: Tajura (Tripolitania, N: 32° 49’ 22.45’’- E: 13° 29’ 39.89’’, 24 m above sea level, north-east Libya), from ruins of abandoned building

Paratypes: (n=129) SNHM-BS40067-70 from Tarunah; SNHM-BS40043-47, 40049-50, 40052, 40054-56, 40058-66 from Msalleta; SNHM-BS39995, 39998, 40001, 40004, 40007-8, 40011-15 from Rass El Lifa; SNHM-BS39933-35,

39937-43, 39995 from El Garbulli; SNHM-BS39944, 39958-59, 40071-40077 from Tajura; SNHM-BS39982-93 from El Sawani; SNHM-BS39960-81; SNHM-BS40016-37, 40039-42 from Garian; SNHM-BS39945, 39949, 39951 from El Sahla; and SNHM-BS40257-84, 40188 from Libya (without precise locality).

Distribution: It is common and widespread in northwestern regions of Libya (Tripolitania, Figure 59). The subspecies has been recorded from the most north western regions, from a variety of habitats. The geckos were collected from high elevations (western mountain, Tarunah, and Msalleta), in these regions the animals were captured from ruins of abandoned buildings, under rocks from valleys, under bridges, from gaps between cement barriers in mountain roads, from caves, also from trees (olive and palm trees). Also the animals were collected from a low elevations in the coastal regions, (from Tajura''15 km to the east of Tripoli'', El Sahla, El Sawani, and El Garbulli), in these regions the geckos were captured from or near human settlements in cities and villages, as well as agricultural zones.

Diagnosis: The new subspecies *T. fascicularis*- complex has a small size: maximum SVL= 77.54 mm versus about the same length 77.72 mm in *T. desert* ssp. nov.- Libya and 82.32 mm in *T. d. deserti* NW-Africa. The number of scales rows around the midbody (10-14, versus 12-14 in *T. desert* ssp. nov.- Libya and 12-13 in *T. d. deserti* NW-Africa) in the same distance; dorsal tubercles giving place to ventral scales without a definite zone of transitional scales as in *T. deserti*; rostral in contact with nostril as in *T. deserti*; tendency for a higher number of subdigital lamellae in the first toe with only a slight overlap 10-12, versus 10-11 in *T. desert* ssp. nov.- Libya, while *T. d. deserti* NW-Africa has a higher number 11-14; a higher number of subdigital lamellae in the fourth toe with overlap 15-18 versus 15-17 in *T. deserti* ssp. nov.- Libya, while *T. d. deserti* NW-Africa has a higher number 16-19; tendency for a higher number of subdigital lamellae in the fifth toe 18-24, versus 19-22 in *T. deserti* ssp. nov.- Libya, while *T. deserti* NW-Africa has a number 21-24. Regarding coloration, there is a diversity of colors; the individuals from coastal regions have

light-brown color, with pattern of pale- brown cross bars run on the dorsal region, while the individuals from mountain regions have brown color, with pattern of dark cross bars run on dorsal region. The new subspecies have more or less the same size as *T. deserti* ssp. nov.- Libya, it is shares with *T. deserti* ssp. nov.- Libya and NW-Africa *T. d. deserti* the condition of dorsal tubercles transitioning to ventral scales without a conspicuous zone of granules; however, the new subspecies differs from *T. deserti* ssp. nov.- Libya and *T. d. deserti* NW-Africa in the range of ventral scales, it was 31-43 versus 38-42 in *T. deserti* ssp. nov.- Libya and 34-37 in *T. d. deserti* NW-Africa. Also new subspecies differs from *T. deserti* ssp. nov. - Libya and NW-Africa *T. d. deserti* in the range number of gular scales; it was 32-53 versus 40-51, and 45-63 in group *T. deserti* ssp. nov.- Libya and *T. deserti* NW-Africa respectively. The new subspecies is covered by oval-shaped, simple central keeled enlarged dorsal tubercles; versus pyramidal, sharply, central keeled dorsal tubercles in *T. deserti*.

Figure 56. Holotype of *Tarentola fascicularis* ssp. nov.- Tajura, Tripolitania-Libya

Description: medium size [SVL: 25.14-77.54 (x=50.22, n=139)]; head length 8.97-24.43 mm (x=16, n=139, head length 31-36% of SVL); head width 5.29-18.5 mm (x=11.54, n=139 head width 60-76% of head length); head Height 2.96-

11.27 mm (x=6.64, n=139, head height 33-46% of head length); eye diameter 1.87-4.92 mm (x=3.33, n=139, eye diameter 20-21% of head length). Dorsum covered by enlarged oval-shaped, simple keeled tubercles arranged in 10-14 (mode 12, n=139) transversal rows at midbody; ventral scales smooth, forming 31-43 (n=139) rows at midbody; interorbital scales 14-16(n=139); 10-12 lamellae underneath of the first toe (n=134); 15-18 lamellae underneath of the fourth toe (n=139); 18-24 lamellae underneath of the fifth toe (n=139).

Description of the Holotype: Snout-vent length: 69.70 mm; tail length: 85.60 ; head length: 22.60 mm; head width: 18.00 mm; head height: 10.00 mm; eye diameter: 4.10 mm; ASL (distance from the front edge of eye up to snout tip): 7.80 mm; AOL (distance from the posterior edge of the eye to the ear opening): 7.20 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:13.90 mm; IOB (interorbital distance): 8.90 mm; FLL: 24.90 mm; HLL: 33.00 mm; HDL: 7.10 mm; HDW: 2.40 mm; FHLL: 33.00 mm; sublabial scales: 8; supralabial scales: 8; IOA (interorbital scales): 15; dorsal tubercles in the axilla-groin distance: 12; ventral scales in the axilla-groin distance: 32; BT:158; 11 lamellae underneath of the first toe ; 15 lamellae underneath of the fourth toe; 19 lamellae underneath of the fifth toe; 44 gular scales from mental scale to gular fold; there is 3 scales that are somehow from the same size as gular scales in contact with mental Cr: 6. Dorsal tubercles are: oval-shaped, simple, central keeled with black spots, and surrounded by a row of secondary tubercles (7-8), of medium size, dorsal tubercles are separated laterally from each other by 2-3 small-size scales, dorsal tubercles on both sides seen more sharply, also on the dorsal side of tail and trend to back . Coloration: basic color of dorsum light-brown, with 5 light-brown cross bars, which extend on to tail as lines (10 light-brown lines), ventral side is white with scattered black dots.

8. *Tarentola* (*Tarentola*) *fascicularis wolfgangi* Joger & Bshaena, 2010.

Holotype: SNHM-BS 41980 (Staatliches Naturhistorisches Museum, Braunschweig), an adult male, collected by Ulrich Joger on 19.08.1998 (Figure 57).

Terra typica: Bou Hedma National Park (Tunisia, N: 34° 24' - E: 9° 23', south-central Tunisia).

Paratypes: (n=33) SNHM-BS39920-39930, 41981, Bou Hedma; HLMD2105-2109, 2265-2271, 2363-2366, Bou Hedma; HLMD1238-1240, Djebel Orbata: El Guettar; ZFMK 49525-49526, Djebel Orbata: El Guettar.

Distribution: So far known from central Tunisia, from Gafsa (Djebel Orbata) in the west to Bou Hedma National Park in the east, south to Degache and Tozeur at northern banks of Chott al Djérid. In these regions the animals were found in rock crevices, on walls and underneath of road bridges; the geckos are active at night.

Derivatio nominis: the subspecies is dedicated to Wolfgang Böhme on the occasion of his retirement as the most successful German curator of herpetology.

Diagnosis: *T. fascicularis wolfgangi* ssp. nov, has small size: maximum SVL=72.3 mm in males, and 57.5 mm in females versus 100 mm in *T. deserti* (male)- NW-Africa, 97 mm in *T. fascicularis. sp* ssp. nov from (Ras Lanuf) northeastern Libya, and 77.54 mm in *T. fascicularis. sp* ssp. nov from (Tripolitania) northwestern Libya. Tail length usually clearly longer than SVL; MOL (ear openings to mental) significantly longer than in *T. fascicularis* and *T. deserti* ssp. nov from north-west Libya (about 90% of head length versus 60-70%); the number of scales rows around the midbody (dorsal tubercles) 11-14 (most often 12), simply keeled (multiply keeled in *T. f. fascicularis* from northeastern Libya and Egypt). Also new subspecies differs from NW-African

T. d. deserti in the range number of gular scales; it was 19-46 versus 45-59 in *T. d. deserti.* Different from all other Tunisian and Libyan *Tarentola* (except *T. neglecta* populations) by lower number of ventral scales (34.3 ±2.7), and lower number of subdigital lamellae underneath 1st and 4th toes (1st 10.3 ±0.8, 4th 15.3 ±1.0). 15-22 scales and lamellae underneath 5th toe versus 16-21 in *T. f. fascicularis*, 21-25 in *T. deserti*). A tendency towards a lower number of interorbital scales comparing with Tunisian *T. mauritanica* (13.7 ±1.0 versus 14.9 ±1.2), and northwestern Libyan *T. fascicularis* ssp.nov (13.7 ±1.0 versus 14.9 ±0.7). Rostral usually not in direct contact with nostril, separated by small scales (unlike in *T. f. fascicularis* where rostral usually in contact with nostril). Regarding coloration, life animals has similar dorsal colour as T. deserti (rosy or yellowish, with yellowish iris, with pattern of five dark transverse bands across back, often reduced to paired spots.

Figure 57. Halotype of *Tarentola fascicularis wolfgangi* ssp. nov, Bou Hedma- south-central Tunisia

Description of the Holotype: Snout-vent length: 61.00 mm; tail length: 71.40 mm; head length: 19.80 mm; head width: 14.70 mm; head height: 10.80 mm; eye diameter: 4.50 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:17.70 mm; IOB (interorbital distance): 8.40 mm; FLL: 23.90 mm; HLL: 30.20 mm; HDL: 5.10 mm; HDW: 2.00 mm; FHLL: 25.10 mm; sublabial scales: 8; supralabial scales: 10; IOA (interorbital

scales): 15; dorsal tubercles in the axilla-groin distance: 12; ventral scales in the axilla-groin distance: 36; 13 lamellae underneath of the first toe ; 15 lamellae underneath of the fourth toe; 20 lamellae underneath of the fifth toe; 43 gular scales from mental scale to gular fold; gular scales separate from mental by 3 scales; Cr (supraorbital scales): 6; 10 supralabials; Dorsal tubercles are: bearing strong central keel from which barely visible keels derive laterally . Coloration: Colour in ethanol whitish, without any visible patterns.

9*. Tarentola* (*Saharogecko*) *neglecta* ssp. nov.-Libya

Holotype: ZCMV 10685, an adult female, collected by Ismail M.Bshaena on October.2008 (Figure 58).

Terra typica: Mandria Oasis (Libyan Sahara desert, N: 26° 45' 40.73''- E: 13° 25' 37.64'', 538 m above sea level, south-west Libya), from abandoned ruins buildings.

Paratypes: (n=2) ZCMV10687-88 from Gaber Aown Oasis (Libyan Sahara desert).

Distribution: it is found in an isolated area inside the Sahara, in south-west desert Oases (Figure 61), the geckos were reported from Gaber Aown Oasis and Mandria Oasis for the first time, the specimens were collected from cracks in ruins of abandoned buildings, and from palm trees.

Diagnosis: *Tarentola neglecta* ssp. nov. has a small size: maximum SVL= 34.76mm versus 59 mm in North-Sahara *T. neglecta neglecta* and 50 mm in Central-Sahara *T. n. geyri* (Joger, 1984a). A tendency towards a higher number of scales rows around the midbody (110, versus 72-98 in *T. n. neglecta, and 93-102 in T. n. geyri*) in the same distance; dorsal tubercles giving place to ventral scales without a definite zone of transitional scales; tendency for a same number of subdigital lamellae in the first toe (10, versus 8-10 in *T. n. neglecta* and 9-10 in *T. n. geyri*); number of subdigital lamellae in the fourth toe (15 versus 12-14 in

T. n. neglecta and 14-15 in *T. n. geyri*); the number of subdigital lamellae in the fifth toe (18, versus 13-15 in *T. n. neglecta*, and 15-18 in *T. n. geyri*), whilst Egyptian *T. mindiae* have an average 16 subdigital lamellae in the fifth toe; a tendency to have the same number of interorbital scales as *T. n. geyri* 12-13 versus 11-12 in *T. n. neglecta*. Regarding coloration, adult individuals have light gray-brown color, with pattern of dark brown near-parallel streaks run on the dorsal region, from the top of head to the tail. The new subspecies shares with *T. neglecta* the small size, and the color pattern; while *T. mindiae* have Light brown color, with pattern of 5-6 blackish bands across back between occiput and sacrum, with two dark near parallel lines run on the snout from the rostral to the interorbital region (Baha El Din, 2006); on the other hand, *T. neglecta* ssp. nov. differs from both subspecies *T. n. neglecta* and *T. n. gyeri*, the new subspecies has a higher number of gular scales (42-52, versus 29-41 in *T. n. neglecta* and 38-40 in *T. n. gyeri*).

Figure 58. Holotype of *Tarentola neglecta* ssp. nov.- Gaber Aown Oasis, southwestern Sahara desert-Libya.

Description: Small in size [SVL: 23.96-34.76 (x=29.36, n=3)], very slim (skinny), with very long tail [tail length about 15% longer than SVL]; with relatively broad head and thin rounded snout, head length 7.11-13.91 mm (x=10.51, n=3, head length 30-40% of SVL); head width 3.98-10.98 mm (x=7.48, n=3, head width 56-79% of head length); head Height 3.22- 6.62 mm (x=4.92, n=3, head height 45-

47% of head length); eye diameter 2.53-3.33 mm (x=2.93, n=3, eye diameter 24-35% of head length). Dorsum covered by enlarged oval-shaped, simple keeled tubercles arranged in 12-13 (n=3) transversal rows at midbody; ventral scales smooth, small in size when compared with dorsal scales, forming 42-43 (n=3) rows at midbody; interorbital scales 12-13 (n=3); 10 lamellae underneath of the first toe (n=3); 15 lamellae underneath of the fourth toe (n=3); and 18 lamellae underneath of the fifth toe (n=3).

Description of the holotype: Snout-vent length: 34.76 mm; head length: 13.91 mm; head width: 10.98 mm; head height: 6.62 mm; eye diameter: 3.33 mm; ASL (distance from the front edge of eye up to snout tip): 5.93 mm; AOL (distance from the posterior edge of the eye to the ear opening): 4.88 mm; MOL (distance from the middle point of the imaginary line between ear openings up to the mental:13.04 mm; IOB (interorbital distance): 6.51 mm; FLL: 18.49 mm; HLL: 24.13 mm; HDL: 4.22 mm; HDW: 1.98 mm; FHLL: 25.38 mm; sublabial scales: 7; supralabial scales: 8; IOA (interorbital scales): 14; dorsal tubercles in the axilla-groin distance: 13; ventral scales in the axilla-groin distance: 42; BT: 110; 10 lamellae underneath of the first toe ; 15 lamellae underneath of the fourth toe; 18 lamellae underneath of the fifth toe; 44 gular scales from mental scale to gular fold; there is 3 scales that are somehow from the same size as gular scales in contact with mental Cr: 5. Dorsal tubercles are: oval-shaped, simple, central keeled with black spots, and is not surrounded by a row of secondary tubercles, dorsal tubercles are separated laterally from each other by 1-2 medium-size scales. Coloration: basic color of dorsum light reddish-brown, with thin dark brown, near-parallel lines or streaks run on the dorsal side (about 5), run on from

snout to sacral region, which linked on the snout to form V-shape, ventral side is white.

Figure 59. Western Mountain (Tripolitania), habitat for *Tarentola fascicularis* ssp. nov.

Figure 60. North-West Tripolitania, habitat for new subspecies *Tarentola deserti* ssp. nov.

Figure 61. Southwestern Sahara desert Oases, habitat for *Tarentola neglecta* ssp. nov.

Figure 62. North-East Libya (Cyrenaica), habitat for *T. f. fascicularis* and *T. fascicularis* ssp. nov. from Taknis

Summary

The genus *Tarentola* (Reptilia: Gekkonidae) consists of about 20 known species, which are distributed mostly in North Africa, coastal regions of Mediterranean Sea, Macaronesian Islands, and also Cuba and the Bahamas. While *Tarentola* of the Canary Islands and Morocco have been very well investigated; we have only little knowledge about the *Tarentola* of the eastern Maghreb countries (Algeria, Tunisia and Libya). The present work is considered as one of the primary studies that are concerned with this genus in North Africa. This study is based on 615 specimens, representative of different forms of the genus *Tarentola*. The specimens were collected through field work from various localities in Libya between 2007-2008, additional specimens of North African *Tarentola* were kindly provided from various collections. In this study, we used both morphological and molecular phylogenetic techniques to investigate the relationships among different populations of the genus *Tarentola* in North Africa.

1- Morphologically, we have extensively analyzed the relationships among different North African *Tarentola* population, the study based on multivariate analysis of 25 external morphological characters (14 morphometric characters and 11 non metric [scalation] characters were used).

2- Molecular phylogenetically, in total 2596 bp DNA sequences were amplified:

A. Two mitochondrial marker genes, partial 12S rRNA (372 bp) and two fragments of 16S rRNA (448 bp and 604 bp respectively).

B. Three nuclear marker genes, the partial *C*-mos (424 bp), the partial RAG2 (387 bp), and fragment of Phosducin (361 bp).

The investigated *Tarentola* sampled through this study (from coastal and desert locations) in Libya demonstrated that, they show a distinct phylogeographical pattern and differ from all other North Africa *Tarentola* populations at least in

some characters, in respect of morphology and mtDNA haplotypes. As a result, the presence of the following monophyletic groups is confirmed:

1- A new subspecies of *T. deserti* from NW-Libya (first record from Libya).

2- A new subspecies of *T. neglecta* from northern central Sahara oases (second record from Libya); *T. mindiae* (only in Egypt) is the sister species of *T. neglecta*.

3- *T. mauritanica* from Morocco, Algeria and Tunisia, not confirmed for Libya.

4- *T. fascicularis* from Egypt, Libya and Tunisia (former subspecies of *T. mauritanica*), comprising five new subspecies from Libya and one new subspecies (*T. fascicularis wolfgangi* Joger and Bshaena 2010) endemic to central Tunisia.

Zusammenfassung

Die Gattung *Tarentola* (Reptilia: Gekkonidae) umfasst etwa 20 bekannte Arten, deren Verbreitung sich häuptsächlich in Nordafrika, mediterranen Küstenregionen und den makaronesischen Inseln erstreckt, die aber auch auf Kuba und den Bahamas vorkommt. Während *Tarentola* auf den Kanaren und in Marokko sehr gut untersucht ist, ist das Wissen über diese Gattung im östlichen Maghreb (umfasst die Staaten Algerien, Tunesien und Libyen) spärlich. Die hier vorliegende Arbeit ist somit eine Pionierstudie an *Tarentola* in Nordafrika. Die Daten für diese Studie stammen von 615 Individuen, die als repräsentativ für die verschiedenen nordafrikanischen Formen dieser Gattung gelten können. Eine Vielzahl der Proben wurden während Feldstudien in den Jahren 2007-2008 an verschiedenen Orten Libyens gesammelt, weitere Proben anderer Länder wurden freundlicherweise aus bereits bestehenden Sammlungen zur Verfügung gestellt. Um in dieser Studie die Verwandtschaftsbeziehungen der verschiedenen beprobten *Tarentola*-Populationen Nordafrikas zu analysieren, wurden sowohl morphologische als auch molekulare Merkmale herangezogen.

1- Morphologische Daten von 25 Merkmalen (14 morphometrische und 11 nicht-metrische Merkmale) wurden mittels multivariaten statistischen Analyen ausgewertet.

2- Molekulare Daten, die insgesamt 2596 bp umfassten, wurden herangezogen. Dies umfasste:

   A. Zwei mitochondriale Marker-Gene: Ein Fragment der 12S rRNA (372 bp) sowie zwei Fragmente von 16S rRNA (je 448 bp und 604 bp).

   B. Drei Kerngene: Ein Fragment von *C*-mos (424 bp), ein RAG2-Fragment (387 bp) sowie ein Fragment des Phosducin-Gens (361 bp).

Es hat sich gezeigt, dass die hier untersuchten *Tarentola* aus den Küsten- und Wüstenregionen Libyens ausgeprägte phylogeographische Muster aufweisen. Sie unterscheiden sich weiterhin von allen anderen nordafrikanischen *Tarentola*-Polulationen, zumindest in einigen morphologischen bzw. mitochondrialen Merkmalen. Darauf beruhend, konnten die folgenden monophyletischen Gruppen definiert werden:

1- Eine neue Unterart von *T. deserti* in NW-Libyen (Erstnachweis in Libyen).

2- Eine neue Unterart von *T. neglecta* aus Oasen der nördlichen mittleren Sahara (zweiter Nachweis in Libyen); *T. mindiae* (auf Ägypten beschränkt) ist die Schwesterart von *T. neglecta*.

3- *T. mauritanica* aus Morokko, Algerien und Tunesien; zu dieser Art gibt es keinen sicheren Nachweis aus Libyen.

4- *T. fascicularis* aus Ägypten, Libyen und Tunesien (zuvor eine Unterart von *T. mauritanica*), die fünf neue Unterarten aus Libyen sowie eine neue Unterart endemisch in Zentraltunesien (*T. fascicularis wolfgangi* Joger and Bshaena 2010) umfasst.

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Appendix 1: List of all Libyan samples, which were collected by the author in the present study

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL001	SNHM-BS 39933	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL002	SNHM-BS 39934	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL003	SNHM-BS 39935	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL004	SNHM-BS 39936	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL005	SNHM-BS 39937	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL006	SNHM-BS 39938	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL007	SNHM-BS 39939	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL008	SNHM-BS 39940	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL009	SNHM-BS 39941	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL010	SNHM-BS 39942	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL011	SNHM-BS 39943	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	20.04.2007
IBL012	SNHM-BS 39944	*Tarentola .sp*	Tajura, 15 km E from Tripoli	an old building	Libya	Ismail. M. Bshaena	21.04.207
IBL013	SNHM-BS 39945	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	abandoned barn	Libya	Ismail. M. Bshaena	24.04.2007
IBL014	SNHM-BS 39946	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	abandoned barn	Libya	Ismail. M. Bshaena	24.04.2007
IBL015	SNHM-BS 39947	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007
IBL016	SNHM-BS 39948	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	abandoned barn	Libya	Ismail. M. Bshaena	24.04.2007
IBL017	SNHM-BS 39949	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007
IBL018	SNHM-BS 39950	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007
IBL019	SNHM-BS 39951	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	abandoned barn	Libya	Ismail. M. Bshaena	24.04.2007
IBL020	SNHM-BS 39952	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007
IBL021	SNHM-BS 39953	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	abandoned barn	Libya	Ismail. M. Bshaena	24.04.2007
IBL022	SNHM-BS 39954	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	abandoned barn	Libya	Ismail. M. Bshaena	24.04.2007
IBL023	SNHM-BS 39955	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007
IBL024	SNHM-BS 39956	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007
IBL025	SNHM-BS 39957	*Tarentola .sp*	El Sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL026	SNHM-BS 39958	*Tarentola .sp*	Tajura, 15 km E from Tripoli	an Old building	Libya	Ismail. M. Bshaena	29.04.2007
IBL027	SNHM-BS 39959	*Tarentola .sp*	Tajura, 15 km E from Tripoli	an Old building	Libya	Ismail. M. Bshaena	29.04.2007
IBL028	SNHM-BS 39960	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL029	SNHM-BS 39961	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL030	SNHM-BS 39962	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL031	SNHM-BS 39963	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL032	SNHM-BS 39964	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL033	SNHM-BS 39965	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL034	SNHM-BS 39966	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL035	SNHM-BS 39967	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL036	SNHM-BS 39968	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL037	SNHM-BS 39969	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	26.04.2007
IBL038	SNHM-BS 39970	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	Under ground abandoned ruins	Libya	Ismail. M. Bshaena	26.04.2007
IBL039	SNHM-BS 39971	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL040	SNHM-BS 39972	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	Under ground abandoned ruins	Libya	Ismail. M. Bshaena	26.04.2007
IBL041	SNHM-BS 39973	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL042	SNHM-BS 39974	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL043	SNHM-BS 39975	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL044	SNHM-BS 39976	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	Under ground abandoned ruins	Libya	Ismail. M. Bshaena	26.04.2007
IBL045	SNHM-BS 39977	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL046	SNHM-BS 39978	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	Under ground abandoned ruins	Libya	Ismail. M. Bshaena	26.04.2007
IBL047	SNHM-BS 39979	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL048	SNHM-BS 39980	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL049	SNHM-BS 39981	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL050	SNHM-BS 39982	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL051	SNHM-BS 39983	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL052	SNHM-BS 39984	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL053	SNHM-BS 39985	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL054	SNHM-BS 39986	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL055	SNHM-BS 39987	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL056	SNHM-BS 39988	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL057	SNHM-BS 39989	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL058	SNHM-BS 39990	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL059	SNHM-BS 39991	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL060	SNHM-BS 39992	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL061	SNHM-BS 39993	*Tarentola .sp*	El sawani, 40 km S from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	27.04.2007
IBL062	SNHM-BS 39994	*Tarentola .sp*	Yafran, 130 Km S from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	26.04.2007
IBL063	SNHM-BS 39995	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	an Old building	Libya	Ismail. M. Bshaena	05.05.2007
IBL064	SNHM-BS 39996	*Tarentola .sp*	El Garbulli, 60 km E from Tripoli	an Old building	Libya	Ismail. M. Bshaena	05.05.2007
IBL065	SNHM-BS 39997	*Tarentola .sp*	El sahla, 38 km SW from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	24.04.2007
IBL066	SNHM-BS 39998	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL067	SNHM-BS 39999	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL068	SNHM-BS 40000	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL069	SNHM-BS 40001	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL070	SNHM-BS 40002	*Tarentola .sp*	Rass El Lifa, South from Tripoli li	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL071	SNHM-BS 40003	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL072	SNHM-BS 40004	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL073	SNHM-BS 40005	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL074	SNHM-BS 40006	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL075	SNHM-BS 40007	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL076	SNHM-BS 40008	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL077	SNHM-BS 40009	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL078	SNHM-BS 40010	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL079	SNHM-BS 40011	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL080	SNHM-BS 40012	*Tarentola .sp*	Rass El Lifa, South from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	25.04.2007
IBL081	SNHM-BS 40013	*Tarentola .sp*	Rass El Lifa, South from Tripoli	From valley ,under bridge in the cement gaps	Libya	Ismail. M. Bshaena	25.04.2007
IBL082	SNHM-BS 40014	*Tarentola .sp*	Rass El Lifa, South from Tripoli	From valley ,under bridge in the cement gaps	Libya	Ismail. M. Bshaena	25.04.2007
IBL083	SNHM-BS 40015	*Tarentola .sp*	Rass El Lifa, South from Tripoli	From valley ,under bridge in the cement gaps	Libya	Ismail. M. Bshaena	25.04.2007
IBL084	SNHM-BS 40016	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL085	SNHM-BS 40017	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL086	SNHM-BS 40018	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL087	SNHM-BS 40019	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL088	SNHM-BS 40020	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL089	SNHM-BS 40021	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL090	SNHM-BS 40022	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL091	SNHM-BS 40023	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL092	SNHM-BS 40024	*Tarentola .sp*	Garian, 80 Km South from Tripoli	In free land in rocky areas (under stones or in clefts)	Libya	Ismail. M. Bshaena	27.04.2007
IBL093	SNHM-BS 40025	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From drains under roads (Mountain roads)	Libya	Ismail. M. Bshaena	27.04.2007
IBL094	SNHM-BS 40026	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From drains under roads (Mountain roads)	Libya	Ismail. M. Bshaena	27.04.2007
IBL095	SNHM-BS 40027	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From drains under roads (Mountain roads)	Libya	Ismail. M. Bshaena	27.04.2007
IBL096	SNHM-BS 40028	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From drains under roads (Mountain roads)	Libya	Ismail. M. Bshaena	27.04.2007
IBL097	SNHM-BS 40029	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From drains under roads (Mountain roads)	Libya	Ismail. M. Bshaena	27.04.2007
IBL098	SNHM-BS 40030	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL099	SNHM-BS 40031	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL100	SNHM-BS 40032	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL101	SNHM-BS 40033	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL102	SNHM-BS 40034	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL103	SNHM-BS 40035	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL104	SNHM-BS 40036	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL105	SNHM-BS 40037	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL106	SNHM-BS 40038	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL107	SNHM-BS 40039	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL108	SNHM-BS 40040	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL109	SNHM-BS 40041	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL110	SNHM-BS 40042	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL111	SNHM-BS 40215	*Tarentola .sp*	Garian, 80 Km South from Tripoli	From the gaps between the cemenrt barriers in the mountain roads	Libya	Ismail. M. Bshaena	27.04.2007
IBL112	SNHM-BS 40216	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL113	SNHM-BS 40217	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL114	SNHM-BS 40218	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL115	SNHM-BS 40219	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL116	SNHM-BS 40220	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL117	SNHM-BS 40221	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL118	SNHM-BS 40222	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL119	SNHM-BS 40223	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL120	SNHM-BS 40224	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL121	SNHM-BS 40043	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL122	SNHM-BS 40044	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL123	SNHM-BS 40045	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL124	SNHM-BS 40046	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL125	SNHM-BS 40047	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL126	SNHM-BS 40048	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL127	SNHM-BS 40049	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL128	SNHM-BS 40050	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL129	SNHM-BS 40051	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL130	SNHM-BS 40052	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL131	SNHM-BS 40053	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL132	SNHM-BS 40054	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL133	SNHM-BS 40055	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL134	SNHM-BS 40056	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL135	SNHM-BS 40057	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL136	SNHM-BS 40058	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL137	SNHM-BS 40059	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL138	SNHM-BS 40060	*Tarentola .sp*	Mselata, 135 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	13.05.2007
IBL139	SNHM-BS 40061	*Tarentola .sp*	Mselata, 135 km E from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	13.05.2007
IBL140	SNHM-BS 40062	*Tarentola .sp*	Mselata, 135 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	13.05.2007
IBL141	SNHM-BS 40063	*Tarentola .sp*	Mselata, 135 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	13.05.2007
IBL142	SNHM-BS 40064	*Tarentola .sp*	Mselata, 135 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	13.05.2007
IBL143	SNHM-BS 40065	*Tarentola .sp*	Mselata, 135 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	13.05.2007
IBL144	SNHM-BS 40066	*Tarentola .sp*	Mselata, 135 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	13.05.2007
IBL145	SNHM-BS 40067	*Tarentola .sp*	Tarunah 95 km SE from Tripoli	From drains under roads (Mountain roads)	Libya	Ismail. M. Bshaena	14.05.2007
IBL146	SNHM-BS 40068	*Tarentola .sp*	Tarunah 95 km SE from Tripoli	In free land in rocky areas (Firm ground, under rocks)	Libya	Ismail. M. Bshaena	14.05.2007
IBL147	SNHM-BS 40069	*Tarentola .sp*	Tarunah 95 km SE from Tripoli	In free land in rocky areas (Firm ground, under rocks)	Libya	Ismail. M. Bshaena	14.05.2007
IBL148	SNHM-BS 40070	*Tarentola .sp*	Tarunah 95 km SE from Tripoli	In free land in rocky areas (Firm ground, under rocks)	Libya	Ismail. M. Bshaena	14.05.2007
IBL149	SNHM-BS 40071	*Tarentola .sp*	Tajura, 36 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	16.05.2007
IBL150	SNHM-BS 40072	*Tarentola .sp*	Tajura, 36 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	16.05.2007
IBL151	SNHM-BS 40073	*Tarentola .sp*	Tajura, 36 km E from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	16.05.2007
IBL152	SNHM-BS 40074	*Tarentola .sp*	Tajura, 36 km E from Tripoli	abandoned ruins buildings	Libya	Ismail. M. Bshaena	16.05.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL153	SNHM-BS 40075	*Tarentola .sp*	Tajura, 36 km E from Tripoli	abandoned baun	Libya	Ismail. M. Bshaena	16.05.2007
IBL154	SNHM-BS 40076	*Tarentola .sp*	Tajura, 36 km E from Tripoli	abandoned baun	Libya	Ismail. M. Bshaena	16.05.2007
IBL155	SNHM-BS 40077	*Tarentola .sp*	Tajura, 36 km E from Tripoli	abandoned baun	Libya	Ismail. M. Bshaena	16.05.2007
IBL156	SNHM-BS 40078	*Tarentola .sp*	Tajura, 36 km E from Tripoli	abandoned baun	Libya	Ismail. M. Bshaena	16.05.2007
IBL157	SNHM-BS 40079	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	an old mud wall	Libya	Ismail. M. Bshaena	15.05.2007
IBL158	SNHM-BS 40080	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	an old mud wall	Libya	Ismail. M. Bshaena	15.05.2007
IBL159	SNHM-BS 40081	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL160	SNHM-BS 40082	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL161	SNHM-BS 40083	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL162	SNHM-BS 40084	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL163	SNHM-BS 40085	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL164	SNHM-BS 40086	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL165	SNHM-BS 40087	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL166	SNHM-BS 40088	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Olive trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL167	SNHM-BS 40089	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL168	SNHM-BS 40090	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL169	SNHM-BS 40091	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL170	SNHM-BS 40092	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL171	SNHM-BS 40093	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL172	SNHM-BS 40094	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL173	SNHM-BS 40095	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL174	SNHM-BS 40096	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL175	SNHM-BS 40097	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL176	SNHM-BS 40098	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL177	SNHM-BS 40099	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL178	SNHM-BS 40100	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL179	SNHM-BS 40101	*Tarentola .sp*	Azzawiyah, 45km W from Tripoli	From Palm trees under crust	Libya	Ismail. M. Bshaena	15.05.2007
IBL180	SNHM-BS 40102	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007
IBL181	SNHM-BS 40103	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	15.05.2007
IBL182	SNHM-BS 40104	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	15.05.2007
IBL183	SNHM-BS 40105	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007
IBL184	SNHM-BS 40225	Tarentola .sp	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007
IBL185	SNHM-BS 40106	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007
IBL186	SNHM-BS 40107	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL187	SNHM-BS 40108	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL188	SNHM-BS 40109	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL189	SNHM-BS 40110	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL190	SNHM-BS 40111	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL191	SNHM-BS 40112	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	an old stone wall	Libya	Ismail. M. Bshaena	17.05.2007
IBL192	SNHM-BS 40113	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	an old stone wall	Libya	Ismail. M. Bshaena	17.05.2007
IBL193	SNHM-BS 40114	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	an old stone wall	Libya	Ismail. M. Bshaena	17.05.2007
IBL194	SNHM-BS 40115	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	an old stone wall	Libya	Ismail. M. Bshaena	17.05.2007
IBL195	SNHM-BS 40116	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL196	SNHM-BS 40117	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	an old stone wall	Libya	Ismail. M. Bshaena	17.05.2007
IBL197	SNHM-BS 40118	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL198	SNHM-BS 40119	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL199	SNHM-BS 40120	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL200	SNHM-BS 40121	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	abandoned ruins buildings	Libya	Ismail. M. Bshaena	17.05.2007
IBL201	SNHM-BS 40122	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007
IBL202	SNHM-BS 40123	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007
IBL203	SNHM-BS 40124	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007
IBL204	SNHM-BS 40125	*Tarentola .sp*	Itwellia, extreme N-W Tripolitania	Old building to store fodder and grain	Libya	Ismail. M. Bshaena	17.05.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL205	SNHM-BS 40126	*Tarentola .sp*	Misratah, 220 East from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	25.05.2007
IBL206	SNHM-BS 40127	*Tarentola .sp*	Misratah, 220 East from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	25.05.2007
IBL207	SNHM-BS 40128	*Tarentola .sp*	Misratah, 220 East from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	25.05.2007
IBL208	SNHM-BS 40129	*Tarentola .sp*	Misratah, 220 East from Tripoli	an Old building	Libya	Ismail. M. Bshaena	25.05.2007
IBL209	SNHM-BS 40130	*Tarentola .sp*	Misratah, 220 East from Tripoli	an Old building	Libya	Ismail. M. Bshaena	17.05.2007
IBL210	SNHM-BS 40131	*Tarentola .sp*	Desert road Ajdabiya& Tobruk	From desert(frim ground, under rocks)	Libya	Ismail. M. Bshaena	22.05.2007
IBL211	SNHM-BS 40132	*Tarentola .sp*	Desert road Ajdabiya& Tobruk	From desert(frim ground, under rocks)	Libya	Ismail. M. Bshaena	22.05.2007
IBL212	SNHM-BS 40133	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL213	SNHM-BS 40134	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL214	SNHM-BS 40135	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL215	SNHM-BS 40136	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL216	SNHM-BS 40137	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL217	SNHM-BS 40138	*Tarentola .sp*	Ras Lanuf, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL218	SNHM-BS 40139	*Tarentola .sp*	Ras Lanuf, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL219	SNHM-BS 40140	*Tarentola .sp*	Ras Lanuf, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL220	SNHM-BS 40141	*Tarentola .sp*	Ras Lanuf, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL221	SNHM-BS 40142	*Tarentola .sp*	Ras Lanuf, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL222	SNHM-BS 40143	*Tarentola .sp*	Marsa El prega, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL223	SNHM-BS 40144	*Tarentola .sp*	Marsa El prega, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL224	SNHM-BS 40145	*Tarentola .sp*	Marsa El prega, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL225	SNHM-BS 40146	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust	Libya	Ismail. M. Bshaena	25.05.2007
IBL226	SNHM-BS 40147	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust	Libya	Ismail. M. Bshaena	25.05.2007
IBL227	SNHM-BS 40148	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust	Libya	Ismail. M. Bshaena	25.05.2007
IBL228	SNHM-BS 40149	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust	Libya	Ismail. M. Bshaena	25.05.2007
IBL229	SNHM-BS 40150	*Tarentola .sp*	Um arrizam, Al Jabel al Akhdar	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL230	SNHM-BS 40151	*Tarentola .sp*	Um arrizam, Al Jabel al Akhdar	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL231	SNHM-BS 40152	*Tarentola .sp*	Um arrizam, Al Jabel al Akhdar	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL232	SNHM-BS 40153	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	an Old building	Libya	Ismail. M. Bshaena	24.05.2007
IBL233	SNHM-BS 40154	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	an Old building	Libya	Ismail. M. Bshaena	24.05.2007
IBL234	SNHM-BS 40155	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	from parcels of beekeeping	Libya	Ismail. M. Bshaena	24.05.2007
IBL235	SNHM-BS 40156	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	from parcels of beekeeping	Libya	Ismail. M. Bshaena	24.05.2007
IBL236	SNHM-BS 40157	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	from parcels of beekeeping	Libya	Ismail. M. Bshaena	24.05.2007
IBL237	SNHM-BS 40158	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	from parcels of beekeeping	Libya	Ismail. M. Bshaena	24.05.2007
IBL238	SNHM-BS 40159	*Hemidactylus turcicue*	Sidi Massod, Al Jabel al Akhdar	an Old building	Libya	Ismail. M. Bshaena	24.05.2007
IBL239	SNHM-BS 40160	*Hemidactylus turcicue*	Sidi Massod, Al Jabel al Akhdar	an Old building	Libya	Ismail. M. Bshaena	24.05.2007
IBL240	SNHM-BS 40161	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	From parcels of beekeeping	Libya	Ismail. M. Bshaena	24.05.2007
IBL241	SNHM-BS 40162	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust	Libya	Ismail. M. Bshaena	5.2007
IBL242	SNHM-BS 40163	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust	Libya	Ismail. M. Bshaena	5.2007
IBL243	SNHM-BS 40164	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust	Libya	Ismail. M. Bshaena	5.2007
IBL244	SNHM-BS 40165	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust	Libya	Ismail. M. Bshaena	5.2007
IBL245	SNHM-BS 40166	*Tarentola .sp*	Taknis, Al Jabel al Akhdar	From trees under crust in rocky area	Libya	Ismail. M. Bshaena	5.2007
IBL246	SNHM-BS 40167	*Tarentola .sp*	Taknis, Al Jabel al Akhdar	From trees under crust in rocky area	Libya	Ismail. M. Bshaena	5.2007
IBL247	SNHM-BS 40168	*Tarentola .sp*	Taknis, Al Jabel al Akhdar	From trees under crust in rocky area	Libya	Ismail. M. Bshaena	5.2007
IBL248	SNHM-BS 40169	*Tarentola .sp*	Taknis, Al Jabel al Akhdar	From trees under crust in rocky area	Libya	Ismail. M. Bshaena	5.2007
IBL249	SNHM-BS 40170	*Tarentola .sp*	Taknis, Al Jabel al Akhdar	From trees under crust in rocky area	Libya	Ismail. M. Bshaena	5.2007
IBL250	SNHM-BS 40171	*Tarentola .sp*	Taknis, Al Jabel al Akhdar	From trees under crust in rocky area	Libya	Ismail. M. Bshaena	5.2007
IBL251	SNHM-BS 40172	*Tarentola .sp*	Taknis, Al Jabel al Akhdar	From trees under crust in rocky area	Libya	Ismail. M. Bshaena	5.2007
IBL252	SNHM-BS 40173	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007
IBL253	SNHM-BS 40174	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007
IBL254	SNHM-BS 40175	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007
IBL255	SNHM-BS 40176	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007
IBL256	SNHM-BS 40226	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL257	SNHM-BS 40227	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007
IBL258	SNHM-BS 40228	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007
IBL259	SNHM-BS 40229	*Tarentola .sp*	Ajdabiya, Cyrenaica	From trees under crust in sandy land area	Libya	Ismail. M. Bshaena	5.2007
IBL260	SNHM-BS 40230	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	25.05.2007
IBL261	SNHM-BS 40231	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	25.05.2007
IBL262	SNHM-BS 40232	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	25.05.2007
IBL263	SNHM-BS 40233	*Tarentola .sp*	Surit, North-Central Libya	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	25.05.2007
IBL264	SNHM-BS 40234	Hemidactylus turcicue	Sidi Massod, Al Jabel al Akhdar	From trees under crust in mountain area	Libya	Ismail. M. Bshaena	25.05.2007
IBL265	SNHM-BS 40235	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	From trees under crust in mountain area	Libya	Ismail. M. Bshaena	24.05.2007
IBL266	SNHM-BS 40236	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	From trees under crust in mountain area	Libya	Ismail. M. Bshaena	24.05.2007
IBL267	SNHM-BS 40237	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	From trees under crust in mountain area	Libya	Ismail. M. Bshaena	24.05.2007
IBL268	SNHM-BS 40238	*Tarentola .sp*	Sidi Massod, Al Jabel al Akhdar	From trees under crust in mountain area	Libya	Ismail. M. Bshaena	24.05.2007
IBL269	SNHM-BS 40239	*Tarentola .sp*	Marsa El prega, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL270	SNHM-BS 40240	*Tarentola .sp*	Marsa El prega, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
IBL271	SNHM-BS 40241	*Tarentola .sp*	Misratah, 220 East from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	25.05.2007
IBL272	SNHM-BS 40242	*Tarentola .sp*	Misratah, 220 East from Tripoli	an Old building	Libya	Ismail. M. Bshaena	25.05.2007
IBL273	SNHM-BS 40243	*Tarentola .sp*	Misratah, 220 East from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	25.05.2007
IBL274	SNHM-BS 40244	*Tarentola .sp*	Misratah, 220 East from Tripoli	an Old building	Libya	Ismail. M. Bshaena	25.05.2007
IBL275	SNHM-BS 40245	*Tarentola .sp*	Misratah, 220 East from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	25.05.2007
IBL276	SNHM-BS 40246	*Tarentola .sp*	Misratah, 220 East from Tripoli	an old stone wall	Libya	Ismail. M. Bshaena	25.05.2007
IBL277	SNHM-BS 40247	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL278	SNHM-BS 40248	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL279	SNHM-BS 40249	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL280	SNHM-BS 40250	*Tarentola .sp*	Tobruk, extreme N-E Cyrenaica	In free land(frim ground)near street Lights at night	Libya	Ismail. M. Bshaena	23.05.2007
IBL281	SNHM-BS 40251	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	5.2007
IBL282	SNHM-BS 40252	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	5.2007

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
IBL283	SNHM-BS 40253	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	5.2007
IBL284	SNHM-BS 40254	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	5.2007
IBL285	SNHM-BS 40255	*Tarentola .sp*	Banghazi, Cyrenaica	From trees under crust in frim land area	Libya	Ismail. M. Bshaena	5.2007
IBL286	SNHM-BS 40256	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL287	SNHM-BS 40177	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL288	SNHM-BS 40178	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL289	SNHM-BS 40179	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL290	SNHM-BS 40180	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL291	SNHM-BS 40181	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL292	SNHM-BS 40182	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL293	SNHM-BS 40183	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL294	SNHM-BS 40184	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL295	SNHM-BS 40185	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL296	SNHM-BS 40186	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL297	SNHM-BS 40187	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL298	SNHM-BS 40188	*Tarentola .sp*	Libya		Libya	Ismail. M. Bshaena	5.2007
IBL299	SNHM-BS 40189	Tarentola .sp	Ras Lanuf, Cyrenaica	abandoned ruins buildings	Libya	Ismail. M. Bshaena	24.05.2007
ZCMV10685	SNHM-BS 42522	*T. neglecta*	Mandria Oasis, SW-Sahara	abandoned mud ruins buildings	Libya	Ismail. M. Bshaena	2008
ZCMV10687	SNHM-BS 42523	*T. neglecta*	Gaber Awon Oasis, SW-Sahara	From tree under crust	Libya	Ismail. M. Bshaena	2008
ZCMV10688	SNHM-BS 42524	*T. neglecta*	Gaber Awon Oasis, SW-Sahara	Abandoned mud ruins buildings	Libya	Ismail. M. Bshaena	2008
ZCMV10690	SNHM-BS 42525	*T. sp*	Tcarkiba, SW-Sahara desert	an old building	Libya	Ismail. M. Bshaena	2008
ZCMV10691	SNHM-BS 42526	*T. sp*	Om Elma Oasis, SW-Sahara	From tree under crust	Libya	Ismail. M. Bshaena	2008
ZCMV10692	SNHM-BS 42527	*T. sp*	El Perkat, SW-Sahara desert	New house under construction	Libya	Ismail. M. Bshaena	2008
ZCMV10701	SNHM-BS 42528	*T. sp*	Sabha, South Libya	In free land in rocky area (firm ground under rocks)	Libya	Ismail. M. Bshaena	2008
ZCMV10703	SNHM-BS 42529	*T. sp*	Sabha, South Libya	In free land in rocky area (firm ground under rocks)	Libya	Ismail. M. Bshaena	2008
ZCMV10704	SNHM-BS 42530	*T. sp*	Germa, South Libya	Abandoned ruins buildings	Libya	Ismail. M. Bshaena	2008

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
ZCMV10706	SNHM-BS 42531	*T. sp*	Sabha, South Libya	In the stall of cattle	Libya	Ismail. M. Bshaena	2008
ZCMV10707	SNHM-BS 42532	*T. sp*	Sabha, South Libya	From a tree under crust	Libya	Ismail. M. Bshaena	2008
ZCMV10708	SNHM-BS 42533	*T. sp*	Sabha, South Libya	an old stone wall	Libya	Ismail. M. Bshaena	2008
ZCMV10710	SNHM-BS 42534	*T. sp*	EL Shwayrif, South Libya	abandoned ruins buildings	Libya	Ismail. M. Bshaena	2008
ZCMV10711	SNHM-BS 42535	*T. sp*	EL Shwayrif, South Libya	an old stone wall	Libya	Ismail. M. Bshaena	2008
ZCMV10712	SNHM-BS 42536	*T. sp*	EL Shwayrif, South Libya	an old stone wall	Libya	Ismail. M. Bshaena	2008
ZCMV10713	SNHM-BS 42537	*T. sp*	EL Shwayrif, South Libya	from a tree under crust	Libya	Ismail. M. Bshaena	2008
ZCMV10714	SNHM-BS 42538	*T. sp*	Bin Ulid, north of Sabha	In free land in rocky area, under rocks	Libya	Ismail. M. Bshaena	2008
ZCMV10715	SNHM-BS 42539	*T. sp*	Bin Ulid, north of Sabha	from a tree under crust	Libya	Ismail. M. Bshaena	2008

Appendix 2: List of the museums samples, which were available for the present study

X= the number of animal is not visible, * = more detailed information not recorded

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
X	SMF-34469	*T. deserti*	Soluk- Cyrenaica	Near see beach	Libya	H. Kaltenbach	6-15.4.1942
X	SMF-34468	*T. deserti*	Soluk- Cyrenaica	Near see beach	Libya	H. Kaltenbach	6-15.4.1942
X	SMF-34467	*T. deserti*	Soluk- Cyrenaica	Near see beach	Libya	H. Kaltenbach	6-15.4.1942
X	SMF-35588	*T. deserti*	Derna- Cyrenaica	*	Libya	W. Stürmer	1.11.1941
TUN 03	SNHM-BS40257	*T. sp*	Bou Hedma	*	Tunisia	Joger.Neubert.Pohl	1999
36019	SNHM-BS 40258	*T. sp*	Bou Hedma	*	Tunisia	Joger	12.08.1998
X	ZFMK-20293	*T.deserti*	Anti Atlas-westTafraont	Anti-Atlas	Morocco	R. Schulte	03.1977
X	ZFMK-49545	*T. mauritanica*	Kerkenna island: Gharbi island	island	Tunisia	W. Bischoff, U. Joger	18.04.1988
X	ZFMK-49546	*T. mauritanica*	Kerkenna island: Gharbi island	island	Tunisia	W. Bischoff, U. Joger	18.04.1988
X	ZFMK-49547	*T. mauritanica*	Kerkenna island: Gharbi island	island	Tunisia	W. Bischoff, U. Joger	18.04.1988
X	ZFMK-49548	*T. mauritanica*	Kerkenna island: Gharbi island	island	Tunisia	W. Bischoff, U. Joger	18.04.1988
X	ZFMK-49549	*T. mauritanica*	Kerkenna island: Gharbi island	island	Tunisia	W. Bischoff, U. Joger	18.04.1988
X	ZFMK-49550	*T. mauritanica*	Kerkenna island: Gharbi island	island	Tunisia	W. Bischoff, U. Joger	18.04.1988
X	ZFMK-34552	*T. mauritanica*	Chafasincis island	island	Morocco	H. H. Witt	10-13.06.1981
X	ZFMK-34553	*T. mauritanica*	Chafasincis island	island	Morocco	H. H. Witt	10-13.06.1981
X	ZFMK-34550	*T. mauritanica*	Chafasincis island	island	Morocco	H. H. Witt	10-13.06.1981
X	ZFMK-34551	*T. mauritanica*	Chafasincis island	island	Morocco	H. H. Witt	10-13.06.1981
X	ZFMK-49638	*T. mauritanica*	Kabylei, near Col de Akfadon	Oak forest	Algeria	W. Bischoff, U. Joger	05.05.1988
X	ZFMK-Nr2	*T. mauritanica*	Algerien	*	Algeria	*	*
X	ZFMK-49620	*T. mauritanica*	Algerien:Belezma.Col de Telmet mountain	*	Algeria	W. Bischoff, U. Joger	02.05.1988
X	ZFMK-49621	*T. mauritanica*	Algerien:Belezma.Col de Telmet mountain	*	Algeria	W. Bischoff, U. Joger	02.05.1988
X	ZFMK-20544	*T. mauritanica*	Algerien	*	Algeria	Frank	1853

Field-Nr	Museum-Nr	Kind (so far)	Locality (collecting sites)	found state	country	Collecting by	date
X	ZFMK-49610	*T. mauritanica*	Algerien.Medracen	*	Algeria	W. Bischoff, U. Joger	01.05.1988
X	ZFMK-20543	*T. mauritanica*	Algeria	*	Algeria	Frank	1853
X	ZFMK-36013	*T. mauritanica*	Algeria:Tiaret	*	Algeria	*	*
X	ZFMK-M1Nr:2	*T. mauritanica*	Algeria	*	Algeria	*	*
38993-6910	X	*T. mauritanica*	*	*	*	*	*
38993-6911	X	*T. mauritanica*	*	*	*	*	*
X	SNHM-BS39912	*T. mauritanica*	H.Atlas.Morocco	*	Morocco	U. Joger	2007
X	SNHM-BS 39913	*T. mauritanica*	H.Atlas.Morocco	*	Morocco	U. Joger	2007
X	ZFMK-49725	*T. mauritanica*	Morocco. 15 KM E- Fes	*	Morocco	W. Bischoff, U. Joger	20.05.1988
X	ZFMK-49702	*T. mauritanica*	Morocco. 8 KM W -Saidia	*	Morocco	W. Bischoff, U. Joger	18.05.1988
X	ZFMK-49822	*T. mauritanica*	Morocco. neighborhood Tanger	*	Morocco	*	*
X	ZFMK-49823	*T. mauritanica*	Morocco. neighborhood Tanger	*	Morocco	*	*
X	ZFMK-46122	*T. mauritanica*	Tunisia:20 Km W- Tozeur	*	Tunisia	G. Vogel	04.1987
X	ZFMK-49515	*T. sp*	Tunisia: Tamerza	*	Tunisia	*	*
X	ZFMK-49516	*T. sp*	Tunisia: Tamerza	*	Tunisia	*	*
X	ZFMK-49517	*T. sp*	Tunisia: Tamerza	*	Tunisia	*	*
X	ZFMK-49525	*T. sp*	Tunisia: Djebel Orbata E El Guettar	Djebel	Tunisia	*	*
X	ZFMK-49526	*T. sp*	Tunisia: Djebel Orbata E El Guettar	Djebel	Tunisia	*	*
X	ZFMK-49784	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988
X	ZFMK-49785	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988
X	ZFMK-49786	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988
X	ZFMK-49787	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988
X	ZFMK-49788	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988
X	ZFMK-49789	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988
X	ZFMK-49790	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
X	ZFMK-49891	*T. m. juliae*	Morocco:Antiatlas, Taroudant	A granite rock	Morocco	W. Bischoff, U. Joger	06.01.1988
X	ZFMK-44073	*T. m. juliae*	SW- Morocco: Taroudant	*	Morocco	H. W. Herrmann	05.06.1985
X	ZFMK-44074	*T. m. juliae*	SW- Morocco: Taroudant	*	Morocco	H. W. Herrmann	05.06.1985
X	ZFMK-44075	*T. m. juliae*	SW- Morocco: Taroudant	*	Morocco	H. W. Herrmann	05.06.1985
X	ZFMK-44076	*T. m. juliae*	SW- Morocco: Taroudant	*	Morocco	H. W. Herrmann	05.06.1985
X	ZFMK-44078	*T. m. juliae*	SW- Morocco: Taroudant	*	Morocco	H. W. Herrmann	05.06.1985
X	ZFMK-49774	*T. m. juliae*	Morocco:30 KM N- Agadir	*	Morocco	W. Bischoff, U. Joger	31.05.1988
X	ZFMK-44085	*T. m. juliae*	SW -Morocco: Bou Izar Karne	*	Morocco	H. W. Herrmann	05.06.1985
X	ZFMK-44082	*T. m. juliae*	SW -Morocco: 2.5 KM E-Taroudant	Of a tree fig	Morocco	H. W. Herrmann	25.05.1985
X	ZFMK-44084	*T. m. juliae*	SW Morocco: 22 KM O Taroudant	Of a tree fig	Morocco	H. W. Herrmann	27.05.1985
X	ZFMK-49756	*T. boehmei*	Morocco: 35 KM SW-Goulimine	*	Morocco	*	*
X	ZFMK-49757	*T. boehmei*	Morocco: 35 KM SW-Goulimine	*	Morocco	*	*
X	ZFMK-49758	*T. boehmei*	Morocco: 35 KM SW-Goulimine	*	Morocco	*	*
X	ZFMK-52473	*T. boehmei*	Morocco: 35 KM SW-Goulimine	*	Morocco	*	*
X	ZFMK-44140	*T. boehmei*	SW- Morocco: 8 KM S- Ait Baha	On a rock	Morocco	H. W. Herrmann	28.06.1985
X	ZFMK-44141	*T. boehmei*	SW- Morocco: 8 KM S- Ait Baha	On a rock	Morocco	H. W. Herrmann	28.06.1985
X	ZFMK-44142	*T. boehmei*	SW- Morocco: 8 KM S- Ait Baha	On a rock	Morocco	H. W. Herrmann	28.06.1985
X	ZFMK-44143	*T. boehmei*	SW- Morocco: 8 KM S- Ait Baha	On a rock	Morocco	H. W. Herrmann	28.06.1985
X	ZFMK-44144	*T. boehmei*	SW- Morocco: 8 KM S- Ait Baha	On a rock	Morocco	H. W. Herrmann	28.06.1985
X	ZFMK-44145	*T. boehmei*	SW- Morocco: 8 KM S- Ait Baha	On a rock	Morocco	H. W. Herrmann	28.06.1985
X	SNHM-BS39914	*T. boehmei*	Morocco: Goulimine	*	Morocco	U.Joger	2004
X	SNHM-BS 39915	*T. boehmei*	Morocco: Bou Jerif, Goulimine	*	Morocco	U.Joger	2004

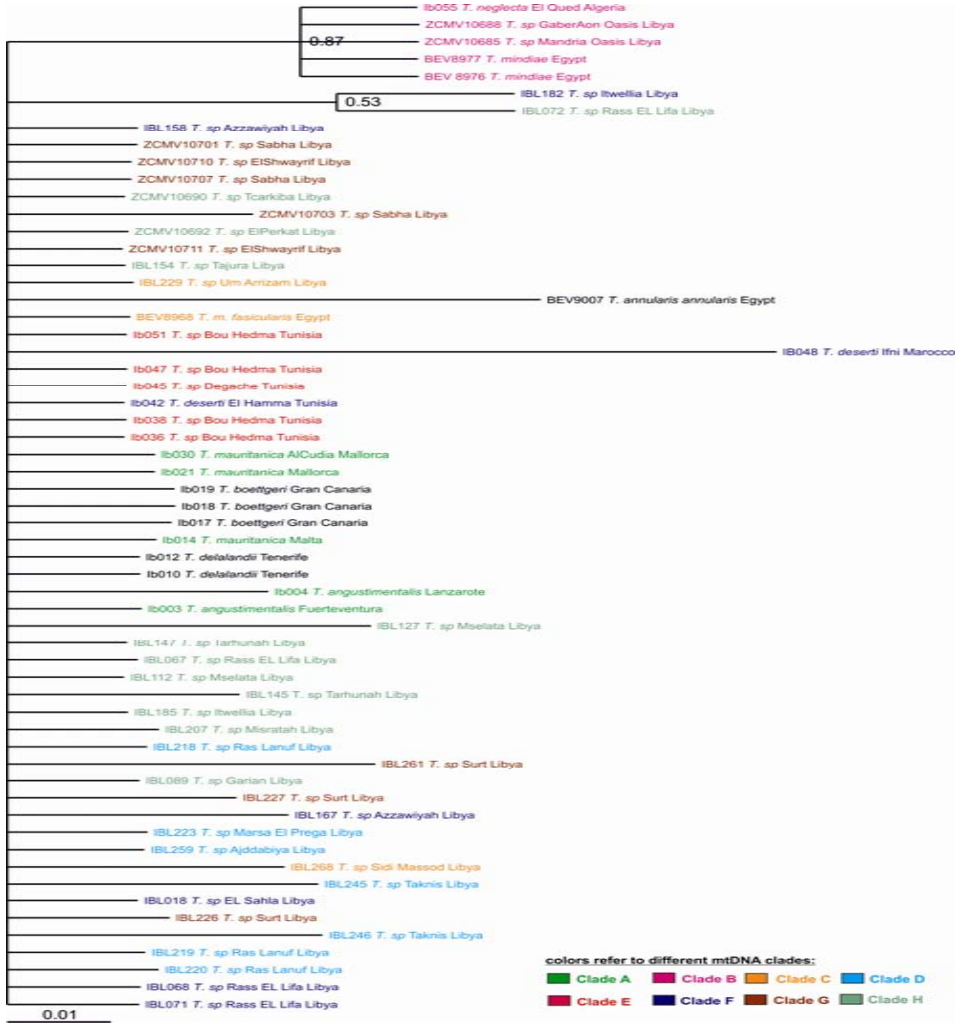
Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
X	SNHM-BS 39916	*T. boehmei*	Morocco: Bou Jerif, Goulimine	*	Morocco	U.Joger	2004
X	SNHM-BS 39917	*T. boehmei*	Morocco: Bou Jerif, Goulimine	*	Morocco	U.Joger	2004
X	SNHM-BS 39918	*T. m. juliae*	Morocco: Ait Baha	*	Morocco	U.Joger	2004
X	SNHM-BS 39919	*T. m. juliae*	Morocco: Ait Baha	*	Morocco	U.Joger	2004
X	ZFMK-2242	*T. deserti*	*	*	*	*	*
X	ZFMK-36618	*T. deserti*	15 km northform Biskra	On a rock	Algeria	U. joger, P. Heimes	11.02.1982
X	ZFMK-38974	*T. deserti*	*	*	*	*	*
X	ZFMK-2238	*T. deserti*	*	*	*	*	*
X	ZFMK-38951	*T. deserti*	Algeria: 10 KM N- Biskra	*	Algeria	Joger & Heizes	1982
X	ZFMK-36619	*T. deserti*	15 km northform Biskra	On a rock	Algeria	U. joger, P. Heimes	11.02.1982
X	ZFMK-2239	*T. deserti*	*	*	*	*	*
X	ZFMK-2241	*T. deserti*	*	*	*	*	*
X	ZFMK-38952	*T. deserti*	Algeria: 10 KM N- Biskra	*	Algeria	Joger & Heizes	1982
X	ZFMK- Nr2	*T. deserti*	*	*	*	*	*
X	ZFMK-2236	*T. deserti*	Ghardaia Oasis	At Mud wall	Algeria	A. Koenig	19.04.1893
X	ZFMK-2244	*T. deserti*	*	*	*	*	*
X	ZFMK-17972	*T. deserti*	Ghardaia: Mzab	*	Algeria	H. E. Back, Ullenbruch	19.05. 1976
X	ZFMK-49578	*T. deserti*	Algeria:10 KM NW El Hamraia	*	Algeria	W. Bischoff, U. Joger	28.04. 1988
X	ZFMK-2232	*T. mauritanica*	El Hobra, north from Quargla	Stony plateau	Algeria	A. Koenig	11-14.4.1893
X	2234	*T. mauritanica*	El Hobra, north from Quargla	Stony plateau	Algeria	A. Koenig	11-14.4.1893
X	ZFMK-49588	*T. deserti*	Algeria: Aures-mountain:Wadi El Hamraia	In Wadi	Algeria	W. Bischoff, U. Joger	29.04.1988
X	ZFMK-6913	*T. deserti*	*	*	*	*	*
X	ZFMK-49587	*T. deserti*	Algeria: Aures-mountain:Wadi El Hamraia	In Wadi	Algeria	W. Bischoff, U. Joger	29.04.1988
X	ZFMK-2235	*T. mauritanica*	El Homra, N-from Quargla	Stony plateau	Algeria	A. Koenig	11-14.4.1893
X	ZFMK-49589	*T. deserti*	Algeria: Aures-mountain:Wadi El Hamraia	In Wadi	Algeria	W. Bischoff, U. Joger	29.04.1988

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
X	ZFMK-2247	*T. deserti*	*	*	*	*	*
X	ZFMK-2237	*T. mauritanica*	Ghardaia Oasis	At Mud wall	Algeria	A. Koenig	19.04.1893
X	ZIBU-17338	*T.m.fascicularis*	Tripolitania	*	Libya	*	*
X	ZIBU-20995	*T.m.fascicularis*	Tripolitania	*	Libya	*	*
X	ZIBU-15434	*T.m.fascicularis*	Tripolitania	*	Libya	*	*
X	ZIBU-15435	*T.m.fascicularis*	Tripolitania	*	Libya	*	*
X	MNHN-1990-1638	*T.m.fascicularis*	Mersa Matrouh	*	Egypt	Hoogstrool	24.09.1954
X	MNHN-1990-1639	*T.m.fascicularis*	Mersa Matrouh	*	Egypt	Hoogstrool	24.09.1954
X	MNHN-1990-1634	*T.m.fascicularis*	Agedabia	*	Libya	schnurrenberger	*
X	MNHN-1990-1633	*T.m.fascicularis*	Agedabia	*	Libya	schnurrenberger	*
X	MNHN-1990-1632	*T.m.fascicularis*	Agedabia	*	Libya	schnurrenberger	*
X	MNHN-1990-1635	*T.m.fascicularis*	Agedabia	*	Libya	schnurrenberger	*
X	MNHN-1990-1631	*T.m.fascicularis*	Agedabia	*	Libya	schnurrenberger	*
X	MNHN-1990-1636	*T.m.fascicularis*	Mersa Matrouh(45 miles W of western desert)- Libya	*	Egypt	Hoogstrool	16.01.1953
X	MNHN-1990-1637	*T.m.fascicularis*	Sidi Barrani (6 miles W of western desert) Egypt	*	Egypt	Hoogstrool	20.04.1954
X	SNHM-BS39920	*T. sp*	*	*	Tunisia	U. Joger	*
X	SNHM-B39921	*T. sp*	*	*	Tunisia	U. Joger	*
X	SNHM-B39922	*T. sp*	*	*	Tunisia	U. Joger	04..09.98-32
X	SNHM-B39923	*T. sp*	Bou Hedma.Tunisia	*	Tunisia	U. Joger	*
X	SNHM-B39924	*T. sp*	Bou Hedma.Tunisia	*	Tunisia	U. Joger	36030
X	SNHM-B39925	*T. sp*	Bou Hedma.Tunisia	*	Tunisia	U. Joger	36030
X	SNHM-B39926	*T. sp*	*	*	Tunisia	U. Joger	32390
X	SNHM-B39927	*T. sp*	Bou Hedma.Tunisia	*	Tunisia	U. Joger	22..09.1987
X	SNHM-B39928	*T. sp*	*	*	Tunisia	U. Joger	*
36027	SNHM-B39929	*T. sp*	Nabeul - Tunisia	*	Tunisia	U. Joger	*
36029	SNHM-B39930	*T. sp*	Bou Hedma.Tunisia	*	Tunisia	U. Joger	*

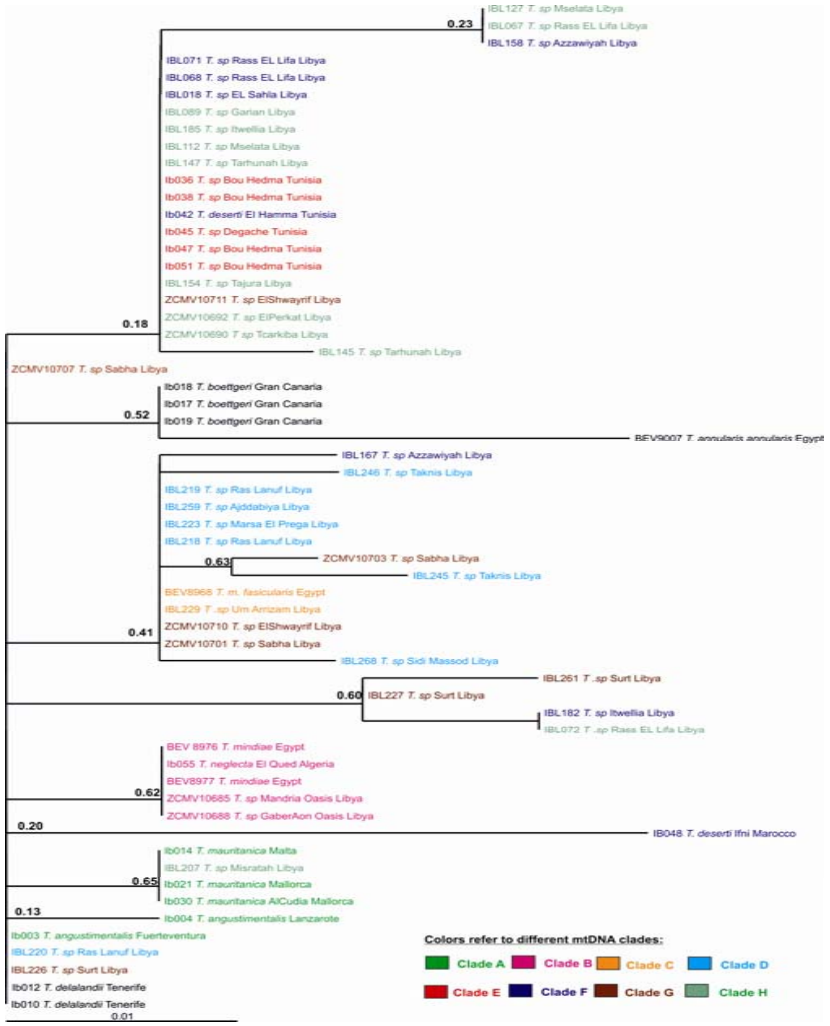
Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
35632	SNHM-B39931	*T. paricarinata*	Terrarium	*	Senegal	U. Joger	*
37320	SNHM-B39932	*T.angustmials*	Lanzarte	*	Canaria Island	U. Joger	*
X	ZFMK-49702	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49705	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49703	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49707	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49704	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49708	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49706	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49709	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-49710	*T. mauritanica*	Saidia	*	Morocco	W.Bischoff, U.Joger	18.05.1988
X	ZFMK-2251	*T. mauritanica*	Monastir: Sousse	*	Tunisia	A.Koenig	03.05.1891
X	ZFMK-2250	*T. mauritanica*	Monastir: Sousse	*	Tunisia	A.Koenig	03.05.1891
X	ZFMK-2225	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	ZFMK-2222	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	ZFMK-2224	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	ZFMK-2226	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	ZFMK-2220	*T. mauritanica*	Mauruba:Tunis	In water pipe	Tunisia	F.Westphal	6.199
X	HLMD-2252	*T. deserti*	Zelfana, 20 km W of it	*	Algeria	U.Joger	28.03.1984
X	ZFMK-2223	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	ZFMK-2219	*T. mauritanica*	Mauruba:Tunis	In water pipe	Tunisia	F.Westphal	6.199
X	ZFMK-2228	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	ZFMK-2231	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	ZFMK-2218	*T. mauritanica*	Mauruba:Tunis	In water pipe	Tunisia	F.Westphal	6.1999
X	ZFMK-2230	*T. mauritanica*	Tunis	Olive tree	Tunisia	A.Koenig	1886/87
X	BEV-8968	*T.m.fasicularis*	Ruinea ballast of the depression of Gatlara, a ballast Maghra	*	Egypt	*	*

Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
X	BEV-8976	*T. mindiae*	East of the depression of qattara, State of Maghra	*	Egypt	*	*
X	BEV-8977	*T. mindiae*	East of the depression of qattara, State of Maghra	*	Egypt	*	*
X	BEV-9007	*T.a. annularis*	Bir Shalatein (extreme SE-. from Egypt, per red)	*	Egypt	*	*
X	T.delalandii 1	*T. delalandii*	Tenriefe	*	Canaria Island	*	*
X	T.delalandii 2	*T. delalandii*	Tenriefe	*	Canaria Island	*	*
X	T.americania III	*T. americania*	Cuba	*	Cuba	*	*
X	T.americania IV	*T. americania*	Cuba	*	Cuba	*	*
1	SNHM-BS40259	*T. m. juliae*	Sous	*	Morocco	Joger	2007
2	SNHM-BS 40260	*T. m. juliae*	Sous	*	Morocco	Joger	2007
3	SNHM-BS 40261	*T. m. juliae*	Sous	*	Morocco	Joger	2007
4	SNHM-BS 40262	*T. m. juliae*	Sous	*	Morocco	Joger	2007
5	SNHM-BS 40263	*T. m. juliae*	Sous	*	Morocco	Joger	2007
6	SNHM-BS 40264	*T. m. juliae*	Sous	*	Morocco	Joger	2007
7	SNHM-BS 40265	*T. m. juliae*	Sous	*	Morocco	Joger	2007
8	SNHM-BS 40266	*T. m. juliae*	Sous	*	Morocco	Joger	2007
9	SNHM-BS 40267	*T. m. juliae*	Sous	*	Morocco	Joger	2007
1	SNHM-BS 40268	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
2	SNHM-BS 40269	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
3	SNHM-BS 40270	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
4	SNHM-BS 40271	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
V	SNHM-BS 40272	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
IV	SNHM-BS 40273	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
5	SNHM-BS 40274	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
6	SNHM-BS 40275	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
7	SNHM-BS 40276	*T. m. juliae*	Imlil	*	Morocco	Joger	2007
X	SNHM-BS 40277	*T. deserti*	Morocco	*	Morocco	Joger	2007

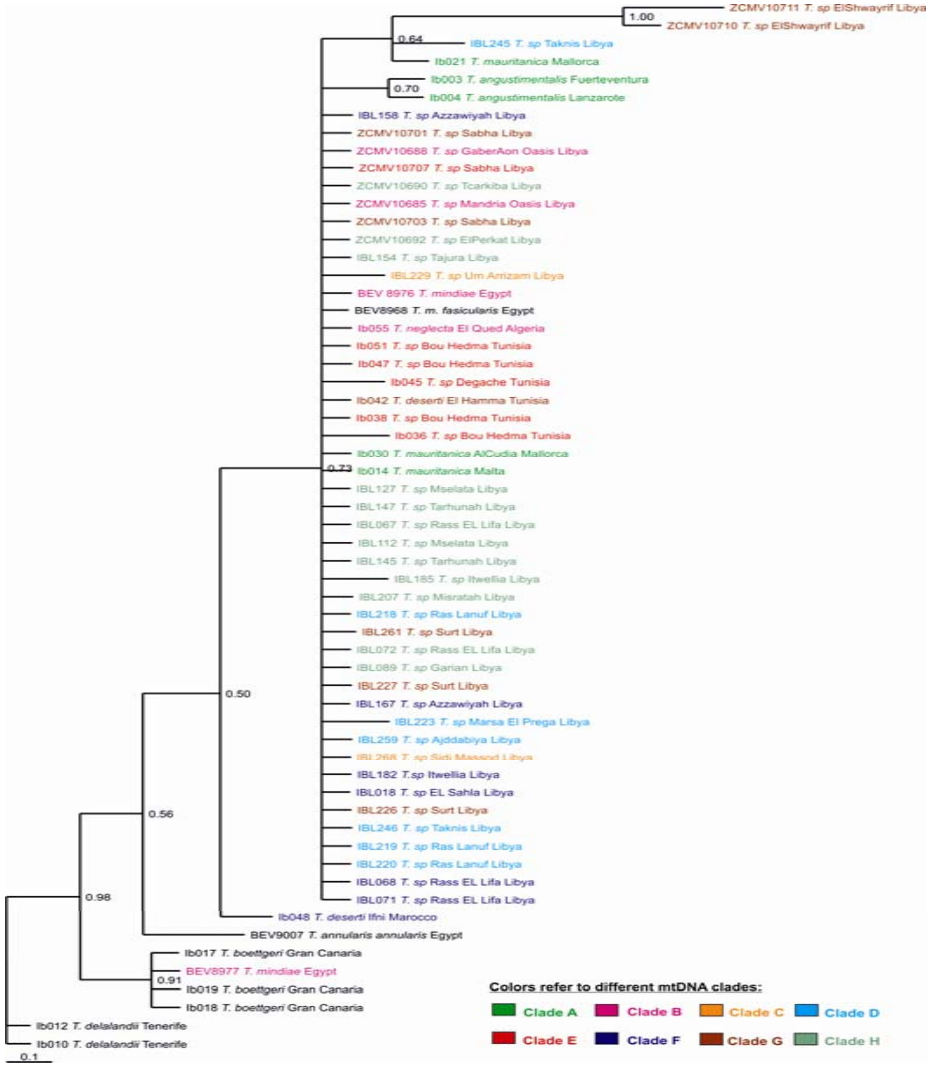
Field-Nr	*Museum-Nr*	*Kind (so far)*	*Locality (collecting sites)*	*found state*	*country*	*Collecting by*	*date*
X	SNHM-BS 40278	*T. boehmei*	Morocco	*	Morocco	Joger	2007
1	SNHM-BS 40279	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
2	SNHM-BS 40280	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
3	SNHM-BS 40281	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
4	SNHM-BS 40282	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
5	SNHM-BS 40283	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
6	SNHM-BS 40284	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
7	SNHM-BS 40285	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
8	SNHM-BS 40286	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
9	SNHM-BS 40287	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*
10	SNHM-BS 40288	*T.m.fascicularis*	Sanai	*	Egypt	Adel Ibrahum	*



Appendix 3. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on 424 bp C-*mos* sequence, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.

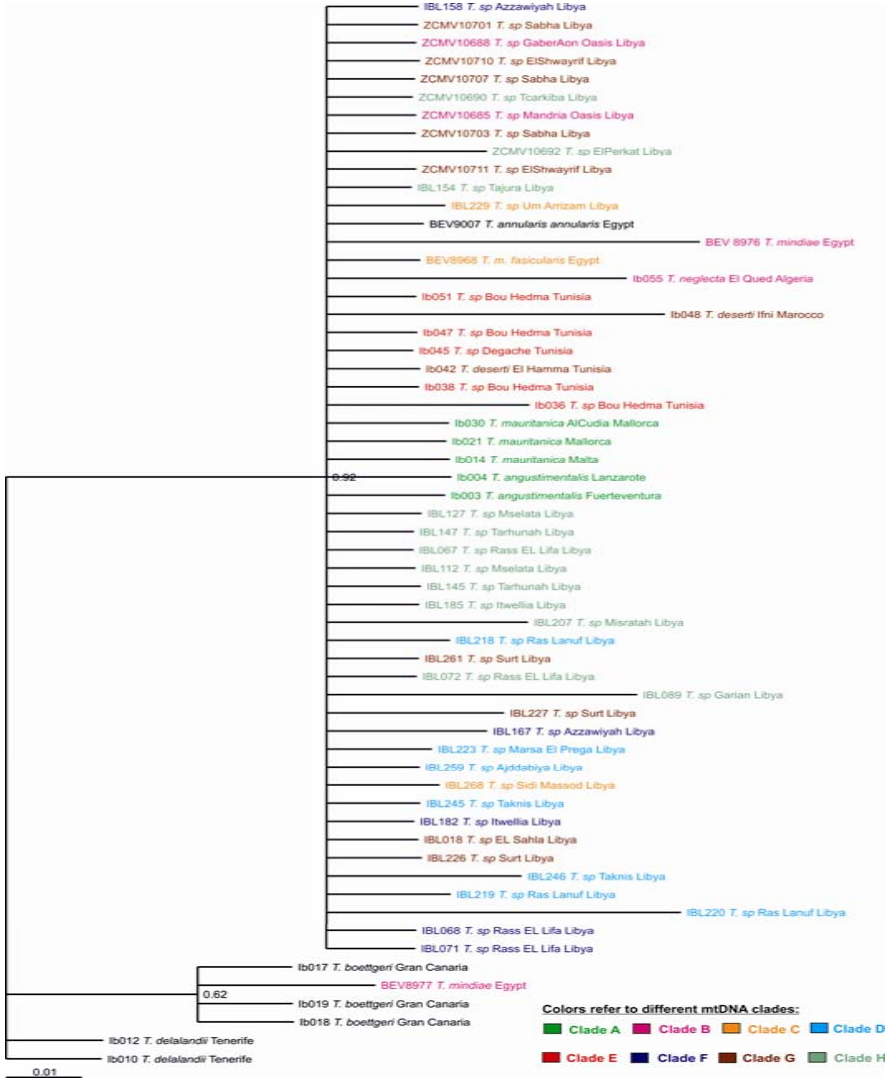


Appendix 4. Tree derived from ML analysis using the model explained in the text, based on 424 bp C-*mos* sequence. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.

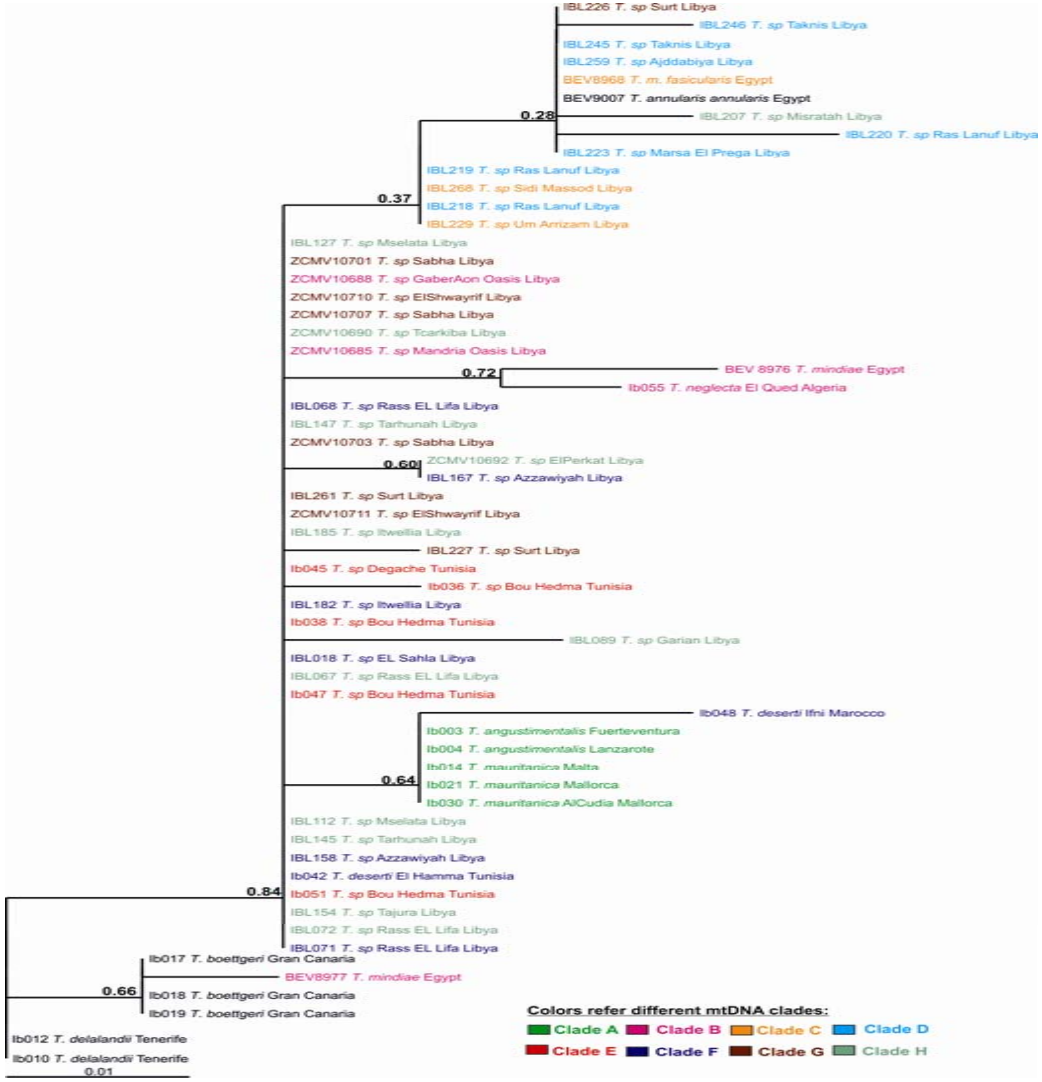


Appendix 5. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on 361 bp Phosducin sequences, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.

Appendix 6. Tree derived from ML analysis using the model explained in the text, based on 361 bp Phosducin sequence. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.



Appendix 7. 50% majority-rule consensus obtained from Bayesian MCMC analysis, using model explained in the text. Based on 387 bp Rag2 sequences, depicting the relationships among haplotypes, with *Tarentola delalandii* designated as outgroup, and Bayesian posterior probability values are given near branches.



Appendix 8. Tree derived from ML analysis using the model explained in the text, based on 387 bp Rag2 sequence. Values near the branches correspond to ML bootstraps values based on 1000 pseudoreplicates, and with *Tarentola delalandii* designated as outgroup.